

1 / 39

1 DIVLTQSPAS LAVSLGQRAT MSCRAGESVD IFGVGFLHWY QOKPGQPPKL  
 51 LIYRASNLIS GIPVRFSGTG SRTDFTLIID PVEADDDVATY YCQQTNEPDY  
 101 TFGGGTKLEI KGGGSGGGG SGGGSGGGG SGGGSGGGG SEVQLQOSGA  
 151 ELVEPGASVK LSCTASGFNI KDTYMHVVKQ RPEQGLEWIG RIDPANGNSK  
 201 YVPKFQ GKAT ITADTSSNTA YLQLTSLTSE DTAVYYCAPF GYYVSDYAMA  
 251 XWGQGTSTTV SS (SEQ ID NO:1)

**FIG.\_1A**

1 GACATCGTCC TGACCCAGAG CCCGGCAAGC CTGGCTGTTT CCCTGGGCCA  
 51 GCGTGCCACT ATGTCCTGCA GAGCGGGTGA GTCTGTTGAC ATTTTCGGTG  
 101 TCGGTTTTCT GCACTGGTAC CAACAGAAAC CGGGTCAGCC GCCAAACTG  
 151 CTGATCTATC GTGCTTCTAA CCTGGAGTCC GGCATCCCGG TACGTTTCTC  
 201 CGGTACTGGC TCTCGTACTG ATTTTACCCT GATTATCGAC CCGGTGGAAG  
 251 CAGACGATGT TGCCACCTAC TATTGCCAGC AGACCAACGA GGATCCGTAC  
 301 ACCTTCGGTG GCGGTACTAA ACTGGAGATC AAAGGCGGTG GTGGTTCTGG  
 351 TGGTGGTGGT AGCGGCGGCG GTGGTAGCGG TGGCGGTGGC AGCGGTGGTG  
 401 GTGGCTCTGG TGGCGGTGGC TCTGAAGTGC AGCTGCAGCA GTCCGGTGCG  
 451 GAGCTCGTTG AACC GGCGC TTCTGTGAAA CTGTCTTGCA CTGCATCTGG  
 501 TTTCAACATT AAGGACACCT ACATGCAC TG GGTGAAACAA CGCCCGGAAC  
 551 AGGGTCTGGA GTGGATCGGT CGCATCGATC CGGCTAACGG TAACAGCAAA  
 601 TACGTGCCAA AATTCCAGGG TAAAGCAACC ATCACTGCTG ATACCTCCTC  
 651 TAACACTGCT TACCTGCAGC TGACTTCCCT GACTAGCGAA GACACCGCGG  
 701 TTTATTACTG CGCTCCGTTT GGCTACTATG TCAGCGATTA CGCAATGGCC  
 751 TACTGGGGTC AGGGCACCTC TGTTACCGTT TCTAGC (SEQ ID NO:3)

**FIG.\_1B**

263 TPVSEKQL AEVVANTITP LMKAQSVPGM AVAVIYQGKP  
 301 HYYTFGKADI AANKPVTPQT LFELGSISKT FTGVLGGDAI ARGEISLDDA  
 351 VTRYWPQLTG KQWQGIRMLD LATYTAGGLP LQVPDEVTDN ASLLRFYQNW  
 401 QPQWKPGTTR LYANASIGLF GALAVKPSGM PYEQAMTTRV LKPLKLDHTW  
 451 INVPKAEEAH YAWGYRDGKA VRVSPGMLDA QAYGVKTNVQ DMANWVMANM  
 501 APENVADASL KQGIALAQSR YWRIGSMYQG LGWEMLNWPV EANTVVETSF  
 551 GNVALAPLPV AEVNPPAPPV KASWVHKTGS TGGFGSYVAF IPEKQIGIVM  
 602 LANTSYPNPA RVEAAYHILE ALQ (SEQ ID NO:11)

**FIG.\_1C**

2 / 39

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1  ACACCGGTGT CAGAAAAACA GCTGGCGGAG GTGGTCGCGA ATACGATTAC
51  CCCGCTGATG AAAGCCCAGT CTGTTCCAGG CATGGCGGTG GCCGTTATTT
101 ATCAGGGAAA ACCGCACTAT TACACATTTG GCAAGGCCGA TATCGCGGCG
151 AATAAACCCG TTACGCCTCA GACCCTGTTC GAGCTGGGTT CTATAAGTAA
201 AACCTTCACC GCGTTTTAG GTGGGGATGC CATTGCTCGC GGTGAAATTT
251 CGCTGGACGA TCGCGTGACC AGATACTGGC CACAGCTGAC GGGCAAGCAG
301 TGGCAGGGTA TTCGTATGCT GGATCTCGCC ACCTACACCG CTGGCGGCCT
351 GCCGCTACAG GTACCGGATG AGGTCACGGA TAACGCCTCC CTGCTGCGCT
401 TTTATCAAAA CTGGCAGCCG CAGTGGAAGC CTGGCACAAC GCGTCTTTAC
451 GCCAACGCCA GCATCGGTCT TTTTGGTGCG CTGGCGGTCA AACCTTCTGG
501 CATGCCCTAT GAGCAGGCCA TGACGACGCG GGTCTTAAG CCGCTCAAGC
551 TGGACCATAC CTGGATTAAC GTGCCGAAAG CGGAAGAGGC GCATTACGCC
601 TGGGGCTATC GTGACGGTAA AGCGGTGCGC GTTTCGCCGG GTATGCTGGA
651 TGCACAAGCC TATGGCGTGA AAACCAACGT GCAGGATATG GCGAACTGGG
701 TCATGGCAAA CATGGCGCCG GAGAACGTTG CTGATGCCTC ACTTAAGCAG
751 GGCATCGCGC TGGCGCAGTC GCGCTACTGG CGTATCGGGT CAATGTATCA
801 GGGTCTGGGC TGGGAGATGC TCAACTGGCC CGTGGAGGCC AACACGGTGG
851 TCGAGACGAG TTTTGGTAAT GTAGCACTGG CGCCGTTGCC CGTGGCAGAA
901 GTGAATCCAC CGGCTCCCCC GGTCAAAGCG TCCTGGGTCC ATAAAACGGG
951 CTCTACTGGC GGGTTTGGA GCTACGTGGC CTTTATTCCT GAAAAGCAGA
1001 TCGGTATTGT GATGCTCGCG AATACAAGCT ATCCGAACCC GGCACGCGTT
1051 GAGGCGGCAT ACCATATCCT CGAGGCGCTA CAG (SEQ ID NO:12)

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**FIG. 1D**

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1  DIVLTQSPAS LAVSLGQRAT MSCRAGESVD IFGVGFLHWY QOKPGOPPKL
51  LIYRASNLIS GIPVRFSGTG SRTDFTLIID PVEADDVATY YCOQTNEDPY
101 TFGGGTKLEI KGGGSGGGG SGGGSGGGG SGGGSGGGG SEVQLQSGA
151 ELVEPGASVK LSCTASGFNI KDTYMHVVKQ RPEQGLEWIG RIDPANGNSK
201 YVPKFQ GKAT ITADTSSNTA YLQLTSLTSE DTAVYYCAPF GYYVSDYAMA
251 YWGQGTSTVTV SSTPVSEKQL AEVVANTITP LMKAQSVPGM AVAVIYQGKP
301 HYYTFGKADI AANKPVTPQT LFELGSISK FTGVLGGDAI ARGEISLDDA
351 VTRYWPQLTG KQWQGIRMLD LATYTAGGLP LQVPDEVTDN ASLLRFYQNW
401 QPQWKPGTTR LYANASIGLF GALAVKPSGM PYEQAMTTRV LKPLKLDHTW
451 INVPKAEAAH YAWGYRDGKA VRVSPGMLDA QAYGVKTNVQ DMANWVMANM
501 APENVADASL KQIALAQSR YWRIGSMYQG LGWEMLNWPV EANTVVETSF
551 GNVALAPLPV AEVNPPAPPV KASVHKGTGS TGGFGSYVAF IPEKQIGIVM
601 LANTSYPNPA RVEAAYHILE ALQ (SEQ ID NO:2)

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**FIG. 1E**

3 / 39

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1   GACATCGTCC TGACCCAGAG CCCGCAAGC CTGGCTGTTT CCCTGGGCCA
51  GCGTGCCACT ATGTCCTGCA GAGCGGGTGA GTCTGTTGAC ATTTTCGGTG
101 TCGGTTTTCT GCACTGGTAC CAACAGAAAC CGGGTCAGCC GCCAAACTG
151 CTGATCTATC GTGCTTCTAA CCTGGAGTCC GGCATCCCGG TACGTTTCTC
201 CGGTACTGGC TCTCGTACTG ATTTTACCCT GATTATCGAC CCGGTGGAAG
251 CAGACGATGT TGCCACCTAC TATTGCCAGC AGACCAACGA GGATCCGTAC
301 ACCTTCGGTG GCGGTACTAA ACTGGAGATC AAAGGCGGTG GTGGTTCCTGG
351 TGGTGGTGGT AGCGGCGGCG GTGGTAGCGG TGGCGGTGGC AGCGGTGGTG
401 GTGGCTCTGG TGGCGGTGGC TCTGAAGTGC AGCTGCAGCA GTCCGGTGCG
451 GAGCTCGTTG AACC GGCGC TTCTGTGAAA CTGTCTTGCA CTGCATCTGG
501 TTTCAACATT AAGGACACCT ACATGCACTG GGTGAAACAA CGCCCGGAAC
551 AGGGTCTGGA GTGGATCGGT CGCATCGATC CGGCTAACGG TAACAGCAAA
601 TACGTGCCAA AATTCCAGGG TAAAGCAACC ATCACTGCTG ATACCTCCTC
651 TAACACTGCT TACCTGCAGC TGACTTCCCT GACTAGCGAA GACACCGCGG
701 TTTATTACTG CGCTCCGTTT GGCTACTATG TCAGCGATTA CGCAATGGCC
751 TACTGGGGTC AGGGCACCTC TGTTACCGTT TCTAGCACAC CGGTGTCAGA
801 AAAACAGCTG GCGGAGGTGG TCGCAATAC GATTACCCCG CTGATGAAAG
851 CCCAGTCTGT TCCAGGCATG GCGGTGGCCG TTATTTATCA GGGAAAACCG
901 CACTATTACA CATTTGGCAA GGCCGATATC GCGGCGAATA AACCCGTTAC
951 GCCTCAGACC CTGTTGAGC TGGGTTCTAT AAGTAAACC TTCACCGCGC
1001 TTTTAGGTGG GGATGCCATT GCTCGCGGTG AAATTTGCT GGACGATGCG
1051 GTGACCAGAT ACTGGCCACA GCTGACGGGC AAGCAGTGGC AGGGTATTCG
1101 TATGCTGGAT CTCGCCACCT ACACCGCTGG CGGCCTGCCG CTACAGGTAC
1151 CGGATGAGGT CACGGATAAC GCCTCCCTGC TCGCTTTTA TCAAACTGG
1201 CAGCCGCAGT GGAAGCCTGG CACAACGCGT CTTTACGCCA ACGCCAGCAT
1251 CGGTCTTTTT GGTGCGCTGG CGGTCAAACC TTCTGGCATG CCCTATGAGC
1301 AGGCCATGAC GACGCGGGTC CTTAAGCCGC TCAAGCTGGA CCATACCTGG
1351 ATTAACGTGC CGAAAGCGGA AGAGGCGCAT TACGCCTGGG GCTATCGTGA
1401 CGGTAAAGCG GTGCGCGTTT CGCCGGGTAT GCTGGATGCA CAAGCCTATG
1451 GCGTGAAAAC CAACGTGCAG GATATGGCGA ACTGGGTCAT GGCAAACATG
1501 GCGCCGAGA ACGTTGCTGA TGCCCTCACTT AAGCAGGGCA TCGCGCTGGC
1551 GCAGTCGCGC TACTGGCGTA TCGGGTCAAT GTATCAGGGT CTGGGCTGGG
1601 AGATGCTCAA CTGGCCCGTG GAGGCCAACA CGGTGGTCGA GACGAGTTTT
1651 GGTAATGTAG CACTGGCGCC GTTGCCCGTG GCAGAAGTGA ATCCACGGC
1701 TCCCCCGGTC AAAGCGTCCT GGGTCCATAA AACGGGCTCT ACTGGCGGGT
1751 TTGGCAGCTA CGTGGCCTTT ATTCCTGAAA AGCAGATCGG TATTGTGATG
1801 CTCGCGAATA CAAGCTATCC GAACCCGGCA CGCGTTGAGG CGGCATACCA
1851 TATCCTCGAG GCGCTACAG (SEQ ID NO:4)

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**FIG. 1F**

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1   DIVLTQSPAS LSVSLGQRAT MSCRAGESVD IFGVGFLHWY QOKPGQPPKL
51  LIYRASNLGS GIPVRFSGTG SGTDFTLIID PVEADDVATY YCQQTNEDPY
101 TFGGGTKLEI KGGGSGGGG SGGGSGGGG SGGGSGGGG SEVQLQSGA
151 ELVEPGASVK LSCTASGFNI KDTYMHVWKQ RPEQGLEWIG RIDPANGNSK
201 YVPKFQKAT ITADTSSNTA YLQLTSLTSE DTAIVYCAPF GYVSDYAMA
251 YWGQTSVTV SS (SEQ ID NO:5)

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**FIG. 2A**

4 / 39

1 GACATCGTCC TGACCCAGAG CCCGGCAAGC CTGTCTGTTT CCCTGGGCCA  
 51 GCGTGCCACT ATGTCCTGCA GAGCGGGTGA GTCTGTTGAC ATTTTCGGTG  
 101 TCGGTTTTCT GCACTGGTAC CAACAGAAAC CGGGTCAGCC GCCAAAAC TG  
 151 CTGATCTATC GTGCTTCTAA CCTGGAGTCC GGCATCCCGG TACGTTTCTC  
 201 CCGTACTGGC TCTGGTACTG ATTTTACCCT GATTATCGAC CCGGTGGAAG  
 251 CAGACGATGT TGCCACCTAC TATTGCCAGC AGACCAACGA GGATCCGTAC  
 301 ACCTTCGGTG GCGGTACTAA ACTGGAGATC AAAGGCGGTG GTGGTTCTGG  
 351 TGGTGGTGGT AGCGGTGGCG GTGGTAGCGG TGGCGGTGGC AGCGGTGGTG  
 401 GTGGCTCTGG TGGCGGTGGC TCTGAAGTGC AGCTGCAGCA GTCCGGTGGC  
 451 GAGCTCGTTG AACC GGCGC TTCTGTGAAA CTGTCTTGCA CTGCATCTGG  
 501 TTTCAACATT AAGGACACCT ACATGCACTG GGTGAAACAA CGCCCGGAAC  
 551 AGGGTCTGGA GTGGATCGGT CGCATCGATC CGGCTAACGG TAACAGCAAA  
 601 TACGTGCCAA AATTCCAGGG TAAAGCAACC ATCACTGCTG ATACCTCCTC  
 651 TAACACTGCT TACCTGCAGC TGACTTCCCT GACTAGCGAA GACACCGCGG  
 701 TTTATTACTG CGCTCCGTTT GGCTACTATG TCAGCGATTA CGCAATGGCC  
 751 TACTGGGGTC AGGGCACCTC TGTTACCGTT TCTAGC (SEQ ID NO:6)

**FIG.\_2B**

262 TPVSEKQL AEVVANTITP LMAAQSVP GM AVAVIYQGKP  
 301 HYYTFGKADI AANKPVTPQT LFELGSISKT FTGVLGGDAI ARGEISLDDA  
 351 VTRYWPQLTG KQWQGIRMLD LATYTAGGLP LQVPDEVTDN ASLLRFYQNW  
 401 QPQWKPGTTR LYANASIGLF GALAVKPSGM PYEQAMTTRV LKPLKLDHTW  
 451 INVPKAEAAH YAWGYRDGKA VRVSPGMLDA QAYGVKTNVQ DMANWVMANM  
 501 APENVADASL KQGIALAQSR YWRIGSMYQG LGWEMLNWPV EANTVVETSF  
 551 GNVALAPLPV AEVNPPAPPV KASWVHKTGS TGGFGAYVAF IPEKQIGIVM  
 601 LANTSYPNPA RVEAAYHILE ALQ (SEQ ID NO:13)

**FIG.\_3**

1 DIVLTQSPAS LSVSLGORAT MSCRAGESVD IFGVGFLHWY QOKPGOPPKL  
51 LIYRASNL ES GIPVRFSGTG SGTDFTLIID PVEADDVATY YCQQTNE D PY  
101 TFGGGTKLEI KGGGSGGGG SGGGSGGGG SGGGSGGGG SEVQLQQSGA  
151 ELVEPGASVK LSCTASGFNI KDTYMHVVKQ RPEQGLEWIG RIDPANGNSK  
201 YVPKFQ GKAT ITADTSSNTA YLQLTSLTSE DTAVYYCAPF GYYVSDYAMA  
251 YWQGTSVTV SSTPVSEKQL AEVVANTITP LMKAQSVP GM AVAVIYQGKP  
 301 HYYTFGKADI AANKPVTPQT LFELGSISKT FTGVLGGDAI ARGEISLDDA  
 351 VTRYWPQLTG KQWQGIRMLD LATYTAGGLP LQVPDEVTDN ASLLRFYQNW  
 401 QPQWKPGTTR LYANASIGLF GALAVKPSGM PYEQAMTTRV LKPLKLDHTW  
 451 INVPKAEAAH YAWGYRDGKA VRVSPGMLDA QAYGVKTNVQ DMANWVMANM  
 501 APENVADASL KQGIALAQSR YWRIGSMYQG LGWEMLNWPV EANTVVETSF  
 551 GNVALAPLPV AEVNPPAPPV KASWVHKTGS TGGFGSYVAF IPEKQIGIVM  
 601 LANTSYPNPA RVEAAYHILE ALQ (SEQ ID NO:7)

**FIG.\_4A**

5 / 39

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1  GACATCGTCC TGACCCAGAG CCCGGCAAGC CTGTCTGTTT CCCTGGGCCA
51  GCGTGCCACT ATGTCCTGCA GAGCGGGTGA GTCTGTTGAC ATTTTCGGTG
101 TCGGTTTTCT GCACTGGTAC CAACAGAAAC CGGGTCAGCC GCCAAAAC TG
151 CTGATCTATC GTGCTTCTAA CCTGGAGTCC GGCATCCCGG TACGTTTCTC
201 CGGTACTGGC TCTGGTACTG ATTTTACCCT GATTATCGAC CCGGTGGAAG
251 CAGACGATGT TGCCACCTAC TATTGCCAGC AGACCAACGA GGATCCGTAC
301 ACCTTCGGTG GCGGTACTAA ACTGGAGATC AAAGGCGGTG GTGGTTCTGG
351 TGGTGGTGGT AGCGGTGGCG GTGGTAGCGG TGGCGGTGGC AGCGGTGGTG
401 GTGGCTCTGG TGGCGGTGGC TCTGAAGTGC AGCTGCAGCA GTCCGGTGCG
451 GAGCTCGTTG AACCGGGCGC TTCTGTGAAA CTGTCTTGCA CTGCATCTGG
501 TTTCAACATT AAGGACACCT ACATGCACTG GGTGAAACAA CGCCCGGAAC
551 AGGGTCTGGA GTGGATCGGT CGCATCGATC CGGCTAACGG TAACAGCAAA
601 TACGTGCCAA AATTCCAGGG TAAAGCAACC ATCACTGCTG ATACCTCCTC
651 TAACACTGCT TACCTGCAGC TGACTTCCCT GACTAGCGAA GACACCGCGG
701 TTTATTACTG CGCTCCGTTT GGCTACTATG TCAGCGATTA CGCAATGGCC
751 TACTGGGGTC AGGGCACCTC TGTTACCGTT TCTAGCACAC CGGTGTGAGA
801 AAAACAGCTG GCGGAGGTGG TCGCGAATAC GATTACCCCG CTGATGAAAG
851 CCCAGTCTGT TCCAGGCATG GCGGTGGCCG TTATTTATCA GGGAAAACCG
901 CACTATTACA CATTTGGCAA GGCCGATATC GCGGCGAATA AACCCGTTAC
951 GCCTCAGACC CTGTTTCGAGC TGGGTTCTAT AAGTAAAACC TTCACCGGCG
1001 TTTTAGGTGG GGATGCCATT GCTCGCGGTG AAATTTTCGCT GGACGATGCG
1051 GTGACCAGAT ACTGGCCACA GCTGACGGGC AAGCAGTGGC AGGGTATTCG
1101 TATGCTGGAT CTCGCCACCT ACACCGCTGG CGGCCTGCCG CTACAGGTAC
1151 CGGATGAGGT CACGGATAAC GCCTCCCTGC TGCCTTTTA TCAAAACTGG
1201 CAGCCGCAGT GGAAGCCTGG CACAACGCGT CTTTACGCCA ACGCCAGCAT
1251 CGGTCTTTTT GGTGCGCTGG CGGTCAAACC TTCTGGCATG CCCTATGAGC
1301 AGGCCATGAC GACGCGGGTC CTTAAGCCGC TCAAGCTGGA CCATACCTGG
1351 ATTAACGTGC CGAAAGCGGA AGAGGCGCAT TACGCCTGGG GCTATCGTGA
1401 CGGTAAAGCG GTGCGCGTTT CGCCGGGTAT GCTGGATGCA CAAGCCTATG
1451 GCGTGAAAAC CAACGTGCAG GATATGGCGA ACTGGGTCAT GGCAAACATG
1501 GCGCCGGAGA ACGTTGCTGA TGCTCACTT AAGCAGGGCA TCGCGCTGGC
1551 GCAGTCGCGC TACTGGCGTA TCGGGTCAAT GTATCAGGGT CTGGGCTGGG
1601 AGATGCTCAA CTGGCCCGTG GAGGCCAACA CGGTGGTTCGA GACGAGTTTT
1651 GGTAATGTAG CACTGGCGCC GTTGCCCGTG GCAGAAGTGA ATCCACCGGC
1701 TCCCCCGGTC AAAGCGTCCT GGGTCCATAA AACGGGCTCT ACTGGCGGGT
1751 TTGGCAGCTA CGTGGCCTTT ATTCCTGAAA AGCAGATCGG TATTGTGATG
1801 CTCGCGAATA CAAGCTATCC GAACCCGGCA CGCGTTGAGG CGGCATACCA
1851 TATCCTCGAG GCGCTACAG (SEQ ID NO:9)
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**FIG. 4B**

6 / 39

1 DIVLTQSPAS LSVSLGORAT MSCRAGESVD IFGVGFLHWY QOKPGOPPKL  
51 LIYRASNLES GIPVRFSGTG SGTDFTLIID PVEADDVATY YCQOTNEDPY  
101 TFGGGTKLEI KGGGSGGGG SGGGSGGGG SGGGSGGGG SEVQLOQSGA  
151 ELVEPGASVK LSCTASGFNI KDTYMHVVKQ RPEOGLEWIG RIDPANGNSK  
201 YVPKFQ GKAT ITADTSSNTA YLQLTSLTSE DTAVYYCAPF GYYVSDYAMA  
251 YWGQTSVTV SSTPVSEKQL AEVVANTITP LMAAQSVPGM AVAVIYQGKP  
301 HYYTFGKADI AANKPVTPTQ LFELGSISK FTGVLGGDAI ARGEISLDDA  
351 VTRYWPQLTG KQWQGIRMLD LATYTAGGLP LQVPDEVTDN ASLLRFYQNW  
401 QPQWKPGTTR LYANASIGLF GALAVKPSGM PYEQAMTTRV LKPLKLDHTW  
451 INVPKAEEAH YAWGYRDGKA VRVSPGMLDA QAYGVKTNVQ DMANWVMANM  
501 APENVADASL KQGIALAQSR YWRIGSMYQG LGWEMLNWPV EANTVVETSF  
551 GNVALAPLPV AEVNPPAPPV KASWVHKTGS TGGFGAYVAF IPEKQIGIVM  
601 LANTSYPNPA RVEAAYHILE ALQ (SEQ ID NO:8)

**FIG.\_4C**

7 / 39

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1   GACATCGTCC TGACCCAGAG CCCGGCAAGC CTGTCTGTTT CCCTGGGCCA
51  GCGTGCCACT ATGTCCTGCA GAGCGGGTGA GTCTGTTGAC ATTTTCGGTG
101 TCGGTTTTCT GCACTGGTAC CAACAGAAAC CGGGTCAGCC GCCAAAAC TG
151 CTGATCTATC GTGCTTCTAA CCTGGAGTCC GGCATCCCGG TACGTTTCTC
201 CGGTACTGGC TCTGGTACTG ATTTTACCCT GATTATCGAC CCGGTGGAAG
251 CAGACGATGT TGCCACCTAC TATTGCCAGC AGACCAACGA GGATCCGTAC
301 ACCTTCGGTG GCGGTACTAA ACTGGAGATC AAAGGCGGTG GTGGTTCTGG
351 TGGTGGTGGT AGCGGTGGCG GTGGTAGCGG TGGCGGTGGC AGCGGTGGTG
401 GTGGCTCTGG TGGCGGTGGC TCTGAAGTGC AGCTGCAGCA GTCCGGTGCG
451 GAGCTCGTTG AACCGGGCGC TTCTGTGAAA CTGTCTTGCA CTGCATCTGG
501 TTTCAACATT AAGGACACCT ACATGCACTG GGTGAAACAA CGCCCGGAAC
551 AGGGTCTGGA GTGGATCGGT CGCATCGATC CGGCTAACGG TAACAGCAAA
601 TACGTGCCAA AATTCCAGGG TAAAGCAACC ATCACTGCTG ATACCTCCTC
651 TAACACTGCT TACCTGCAGC TGACTTCCCT GACTAGCGAA GACACCGCGG
701 TTTATTACTG CGCTCCGTTT GGCTACTATG TCAGCGATTA CGCAATGGCC
751 TACTGGGGTC AGGGCACCTC TGTTACCGTT TCTAGCACAC CGGTGTCAGA
801 AAAACAGCTG GCGGAGGTGG TCGCGAATAC GATTACCCCG CTGATGGCGG
851 CCCAGTCTGT TCCAGGCATG GCGGTGGCCG TTATTTATCA GGGAAAACCG
901 CACTATTACA CATTTGGCAA GGCCGATATC GCGGCGAATA AACCCGTAC
951 GCCTCAGACC CTGTTGAGC TGGGTCTTAT AAGTAAAACC TTCACCGGCG
1001 TTTTAGGTGG GGATGCCATT GCTCGCGGTG AAATTTTCGCT GGACGATGCG
1051 GTGACCAGAT ACTGGCCACA GCTGACGGGC AAGCAGTGGC AGGGTATTTCG
1101 TATGCTGGAT CTCGCCACCT ACACCGCTGG CGGCCTGCCG CTACAGGTAC
1151 CGGATGAGGT CACGGATAAC GCCTCCCTGC TCGCCTTTTA TCAAAACTGG
1201 CAGCCGCACT GGAAGCCTGG CACAACGCGT CTTTACGCCA ACGCCAGCAT
1251 CGGTCTTTTT GGTGCGCTGG CGGTCAAACC TTCTGGCATG CCTATGAGC
1301 AGGCCATGAC GACGCGGGTC CTTAAGCCGC TCAAGCTGGA CCATACCTGG
1351 ATTAACGTGC CGAAAGCGGA AGAGGCGCAT TACGCTGGG GCTATCGTGA
1401 CGGTAAAGCG GTGCGCGTTT CGCCGGGTAT GCTGGATGCA CAAGCCTATG
1451 GCGTGAAAAC CAACGTGCAG GATATGGCGA ACTGGGTCAT GGCAAACATG
1501 GCGCCGGAGA ACGTTGCTGA TGCCTCACTT AAGCAGGGCA TCGCGCTGGC
1551 GCAGTCGCGC TACTGGCGTA TCGGGTCAAT GTATCAGGGT CTGGGCTGGG
1601 AGATGCTCAA CTGGCCCGTG GAGGCCAACA CCGTGGTGCA GACGAGTTTT
1651 GGTAATGTAG CACTGGCGCC GTTGCCCGTG GCAGAAAGTGA ATCCACCGGC
1701 TCCCCCGGTC AAAGCGTCCT GGGTCCATAA AACGGGCTCT ACTGGCGGGT
1751 TTGGCGCGTA CGTGGCCTTT ATTCCTGAAA AGCAGATCGG TATTGTGATG
1801 CTCGCGAATA CAAGCTATCC GAACCCGGCA CGCGTTGAGG CGGCATACCA
1851 TATCCTCGAG GCGCTACAG (SEQ ID NO:10)

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**FIG.\_4D**

8 / 39

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1   AGGAATTATC ATATGAAATA CCTGCTGCCG ACCGCTGCTG CTGGTCTGCT
51  GCTCCTCGCT GCCCAGCCGG CCATGGCCGA CATCGTCCTG ACCCAGAGCC
101 CGGCAAGCCT GTCTGTTTCC CTGGGCCAGC GTGCCACTAT GTCCTGCAGA
151 GCGGGTGAGT CTGTTGACAT TTTCGGTGTC GGTTTTCTGC ACTGGTACCA
201 ACAGAAACCG GGTGAGCCGC CAAAACTGCT GATCTATCGT GCTTCTAACC
251 TGGAGTCCGG CATCCCAGTA CGTTTCTCCG GTACTGGCTC TGGTACTGAT
301 TTTACCCTGA TTATCGACCC GGTGGAAGCA GACGATGTTG CCACCTACTA
351 TTGCCAGCAG ACCAACGAGG ATCCGTACAC CTTCCGGTGGC GGTACTAAAC
401 TGGAGATCAA AGGCGGTGGT GGTTCCTGGT GTGGTGGTAG CGGTGGCGGT
451 GGTAGCGGTG GCGGTGGCAG CGGTGGTGGT GGCTCTGGTG GCGGTGGCTC
501 TGAAGTGCAG CTGCAGCAGT CCGGTGCGGA GCTCGTTGAA CCGGGCGCTT
551 CTGTGAAACT GTCTTGCACT GCATCTGGTT TCAACATTAA GGACACCTAC
601 ATGCACTGGG TGAAACAACG CCCGGAACAG GGTCTGGAGT GGATCGGTCTG
651 CATCGATCCG GCTAACGGTA ACAGCAAATA CGTGCCAAAA TTCCAGGGTA
701 AAGCAACCAT CACTGCTGAT ACCTCCTCTA ACACTGCTTA CCTGCAGCTG
751 ACTTCCCTGA CTAGCGAAGA CACCGCGGTT TATTACTGCG CTCCGTTCCG
801 CTACTATGTC AGCGATTACG CAATGGCCTA CTGGGGTCAG GGCACCTCTG
851 TTACCGTTTC TAGCACACCG GTGTCAGAAA AACAGCTGGC GGAGGTGGTC
901 GCGAATACGA TTACCCCGCT GATGGCGGCC CAGTCTGTTC CAGGCATGGC
951 GGTGGCCGTT ATTTATCAGG GAAAACCGCA CTATTACACA TTTGGCAAGG
1001 CCGATATCGC GGCGAATAAA CCCGTTACGC CTCAGACCCT GTTCGAGCTG
1051 GGTTCTATAA GTAAAACCTT CACCGGCGTT TTAGGTGGGG ATGCCATTGC
1101 TCGCGGTGAA ATTTGCTGG ACGATGCGGT GACCAGATAC TGGCCACAGC
1151 TGACGGGCAA GCAGTGGCAG GGTATTCGTA TGCTGGATCT CGCCACCTAC
1201 ACCGCTGGCG GCCTGCCGCT ACAGGTACCG GATGAGGTCA CGGATAACGC
1251 CTCCCTGCTG CGCTTTTATC AAAACTGGCA GCCGAGTGG AAGCCTGGCA
1301 CAACGCGTCT TTACGCCAAC GCCAGCATCG GTCTTTTGG TGCGCTGGCG
1351 GTCAAACCTT CTGGCATGCC CTATGAGCAG GCCATGACGA CGCGGGTCC
1401 TAAGCCGCTC AAGCTGGACC ATACCTGGAT TAACGTGCCG AAAGCGGAAG
1451 AGGCGCATTA CGCCTGGGGC TATCGTGACG GTAAAGCGGT GCGCGTTTCG
1501 CCGGGTATGC TGGATGCACA AGCCTATGGC GTGAAAACCA ACGTGCAGGA
1551 TATGGCGAAC TGGGTCATGG CAAACATGGC GCCGAGAAC GTTGCTGATG
1601 CCTCACTTAA GCAGGGCATC GCGCTGGCGC AGTCGCGCTA CTGGCGTATC
1651 GGGTCAATGT ATCAGGGTCT GGGCTGGGAG ATGCTCAACT GGCCCGTGGA
1701 GGCCAACACG GTGGTCGAGA CGAGTTTGG TAATGTAGCA CTGGCGCCGT
1751 TGCCCGTGGC AGAAGTGAAT CCACCGGCTC CCCCAGTCAA AGCGTCCTGG
1801 GTCCATAAAA CGGGCTCTAC TGGCGGGTTT GCGCGGTACG TGGCCTTTAT
1851 TCCTGAAAAG CAGATCGGTA TTGTGATGCT CGCGAATACA AGCTATCCGA
1901 ACCCGGCACG CGTTGAGGCG GCATACCATA TCCTCGAGGC GCTACAGTAG
1951 GAATTGAGC TCCGTCGACA AGCTTGCGGC CGCACTCGAG ATCAAACGGG
2001 CTAGCCAGCC AGAACTCGCC CCGGAAGACC CCGAGGATGT CGAGCACCAC
2051 CACCACCACC ACTGAGATCC GGCTGCTAAC AAAGCCCGAA AGGAAGCTGA
2101 GTTGCGTGC T GCCACCGCTG AGCAATAACT AGCATAACCC CTTGGGGCCT
2151 CTAAACGGGT CTTGAGGGGT TTTTGTGCTGA AAGGAGGAAC TATATCCGGA
2201 TTGGCGAATG GGACGCGCCC TGTAGCGGCG CATTAAGCGC GGCGGGTGTG
2251 GTGGTTACGC GCAGCGTGAC CGTACACTT GCCAGCGCCC TAGCGCCCGC
2301 TCCTTTCGCT TTCTTCCCTT CCTTCTCGC CACGTTCCGC GGCTTTCCTC

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**FIG. 4E-1**

SUBSTITUTE SHEET (RULE 26)



9 / 39

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2351 GTCAAGCTCT AAATCGGGGG CTCCCTTTAG GGTTCGATT TAGTGCTTTA
2401 CGGCACCTCG ACCCAA AAAA ACTTGATTAG GGTGATGGTT CACGTAGTGG
2451 GCCATCGCCC TGATAGACGG TTTTTCGCCC TTTGACGTTG GAGTCACGT
2501 TCTTTAATAG TGGACTCTTG TTCCAAACTG GAACAACACT CAACCCTATC
2551 TCGGTCTATT CTTTGTATTT ATAAGGGATT TTGCCGATTT CGGCC TATTG
2601 GTTAAAAAAT GAGCTGATTT AACAAAAATT TAACGCGAAT TTAA CAAAA
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2701 GCGGTATTTT ACACCGCATA TGGTGCACCTC TCAGTACAAT CTGCTCTGAT
2751 GCCGCATAGT TAAGCCAGCC CCGACACCCG CCAACACCCG CTGACGCGCC
2801 CTGACGGGCT TGTCTGCTCC CGGCATCCGC TTACAGACAA GCTGTGACCG
2851 TCTCCGGGAG CTGCATGTGT CAGAGGTTTT CACCGTCATC ACCGA AACGC
2901 GCGAGACGAA AGGGCCTCGT GATACGCCTA TTTTATAGG TTAATGTCAT
2951 GATAATAATG GTTCTTTAGA CGTCAGGTGG CACTTTTCGG GGAATGTGC
3001 GCGGAACCCC TATTTGT TTA TTTTCTAAA TACATTCAA TATGTATCCG
3051 CTCATGAGAC AATAACCTG TGGCAGCATC ACCCGACGCA CTTTGCGCCG
3101 AATAAATACC TGTGACGGAA GATCACTTCG CAGAATAAAT AAATCCTGGT
3151 GTCCCTGTTG ATACCGGGAA GCCCTGGGCC AACTTTTGGC GAAAATGAGA
3201 CGTTGATCGG CACGTAAGAG GTTCCAACCT TCACCATAAT GAAATAAGAT
3251 CACTACCGGG CGTATTT TTT GAGTTATCGA GATTTTCAGG AGCTAAGGAA
3301 GCTAAAATGG AGAAAAAAT CACTGGATAT ACCACCGTTG ATATATCCCA
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4001 AGCATTGGTA ACTGTCAGAC CAAGTTTACT CATATATACT TTAGATTGAT
4051 TTAAAACCTC ATTTT TAAAT TAAAAGGATC TAGGTGAAGA TCTTTT TGA
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4151 CAGACCCCGT AGAAAAGATC AAAGGATCTT CTTGAGATCC TTTT TCTG
4201 CGCGTAATCT GCTGCTTGCA AACAAAAAAA CCACCGCTAC CAGCGGTGGT
4251 TTGTTTGCCG GATCAAGAGC TACCAACTCT TTTTCCGAAG GTA ACTGGCT
4301 TCAGCAGAGC GCAGATACCA AATACTGTTC TTCTAGTGTA GCCGTAGTTA
4351 GGCCACCACT TCAAGAACTC TGTAGCACCG CCTACATACC TCGCTCTGCT
4401 AATCCTGTTA CCAGTG GCTG CTGCCAGTGG CGATAAGTCG TGTCTTACCG
4451 GGTTGGACTC AAGACGATAG TTACCGGATA AGGCGCAGCG GTCGGGCTGA
4501 ACGGGGGGTT CGTGCA CACA GCCCAGCTTG GAGCGAACGA CCTACACCGA
4551 ACTGAGATAC CTACAGCGTG AGCTATGAGA AAGCGCCACG CTTCCCGAAG
4601 GGAGAAAGGC GGACAGGTAT CCGGTAAGCG GCAGGGTCCG AACAGGAGAG
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**FIG. 4E-2**

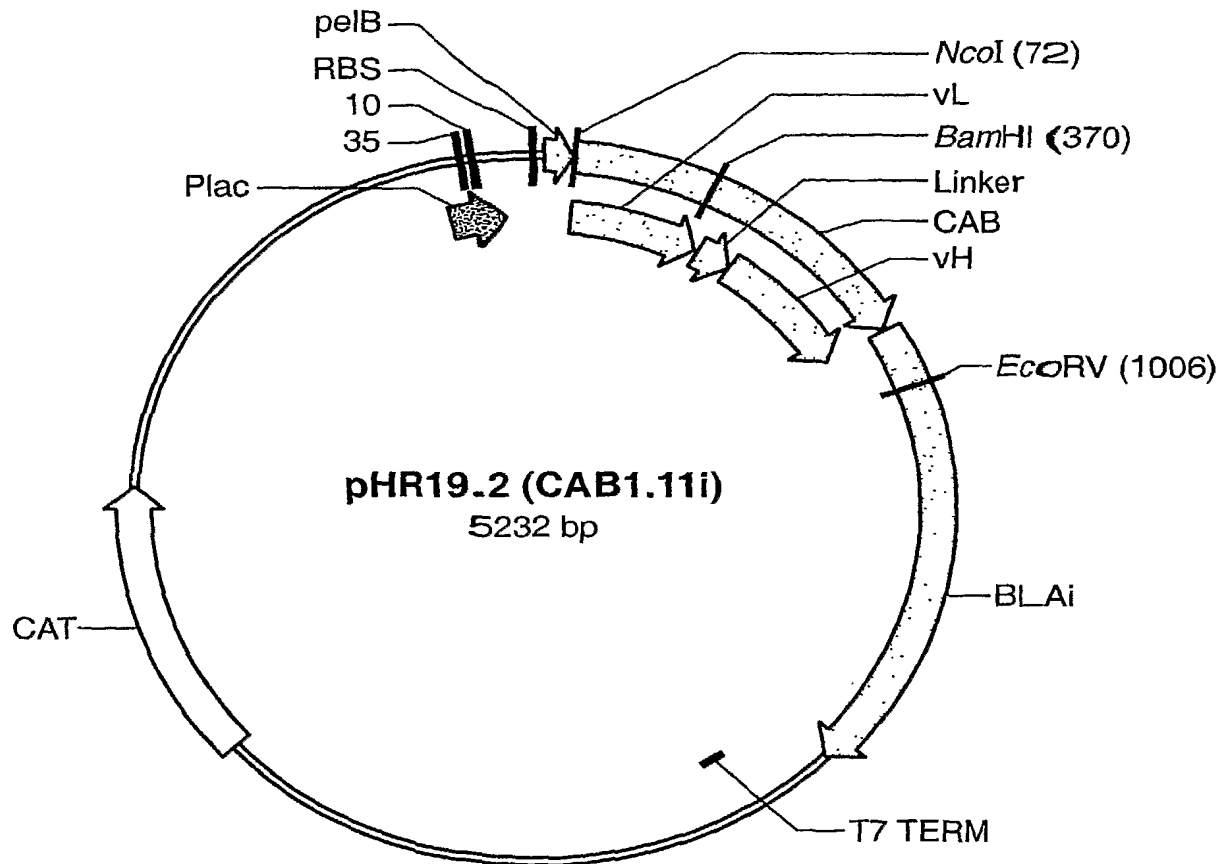
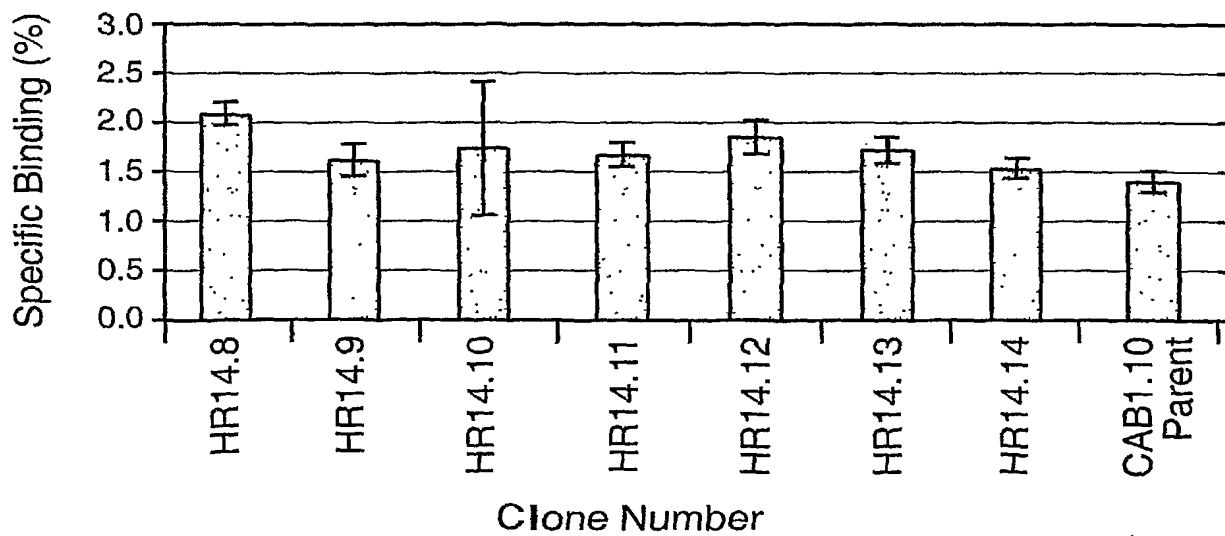
SUBSTITUTE SHEET (RULE 26)

10/39

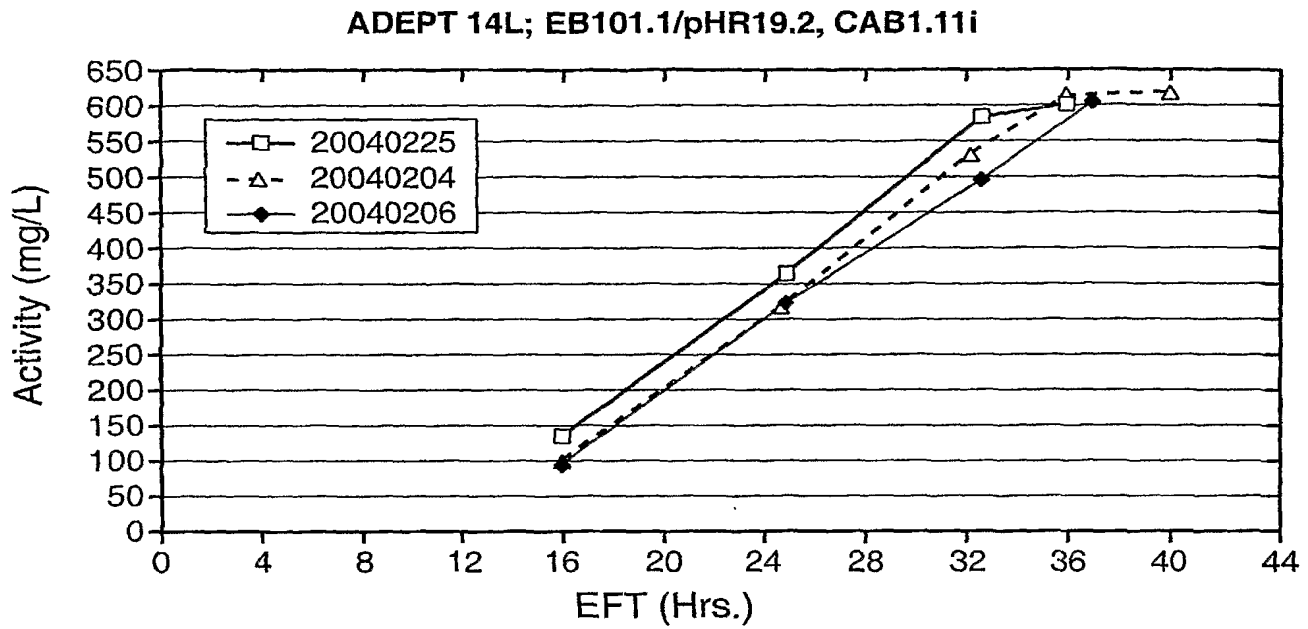
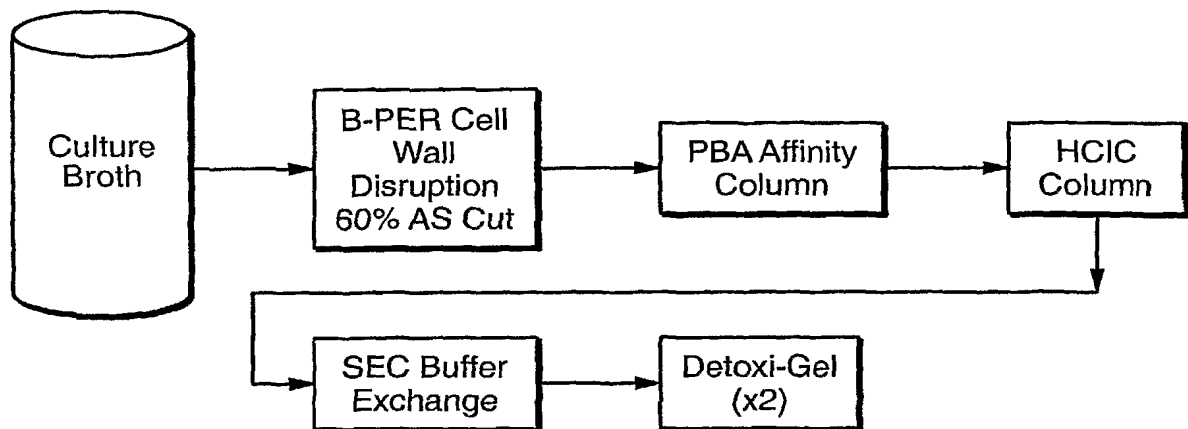
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4851 TGATTCTGTG GATAACCGTA TTACCGCCTT TGAGTGAGCT GATACCGCTC  
4901 GCCGCAGCCG AACGACCGAG CGCAGCGAGT CAGTGAGCGA GGAAGCGGAA  
4951 GAGCGCCCAA TACGCAAACC GCCTCTCCCC GCGCGTTGGC CGATTCATTA  
5001 ATGCAGCTGG CACGACAGGT TTCCCGACTG GAAAGCGGGC AGTGAGCGCA  
5051 ACGCAATTAA TGTGAGTTAG CTCACTCATT AGGCACCCCA GGCTTTACAC  
5101 TTTATGCTTC CGGCTCGTAT GTTGTGTGGA ATTGTGAGCG GATAACAATT  
5151 TCACACAGGA AACAGCTATG ACCATGATTA CGCCAAGCTA TTTAGGTGAC  
5201 ACTATAGAAT ACTCAAGCTT TCTAGATTAA GG

**FIG. 4E-3**

11 / 39

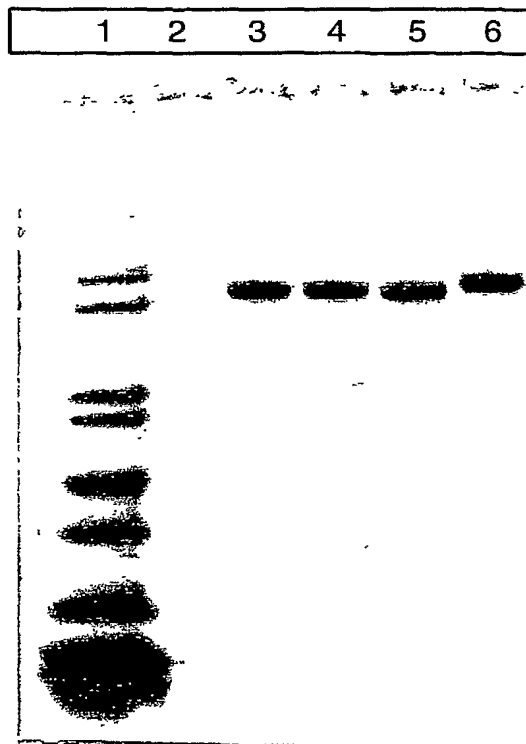
**FIG.\_5****FIG.\_6**

12 / 39

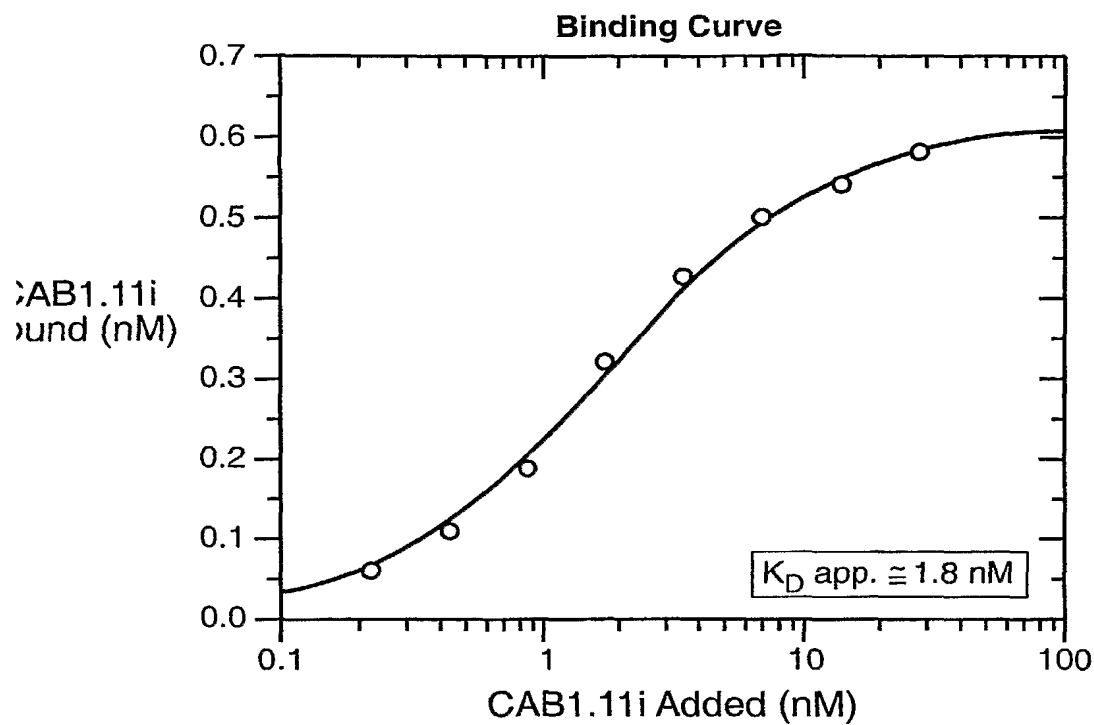
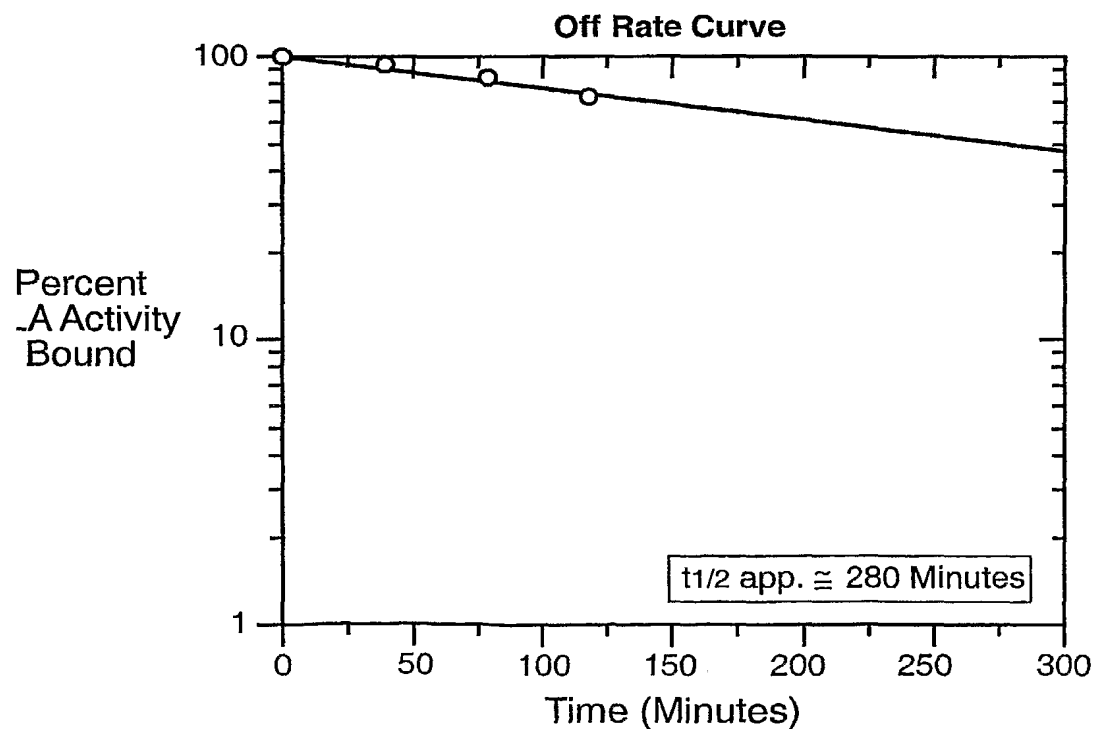
**FIG. 7****FIG. 8**

13 / 39

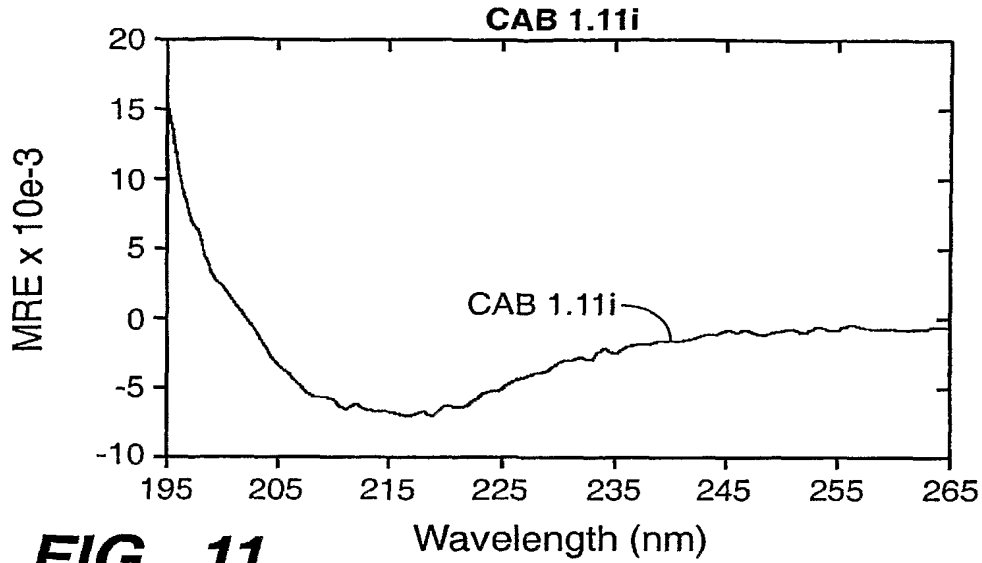
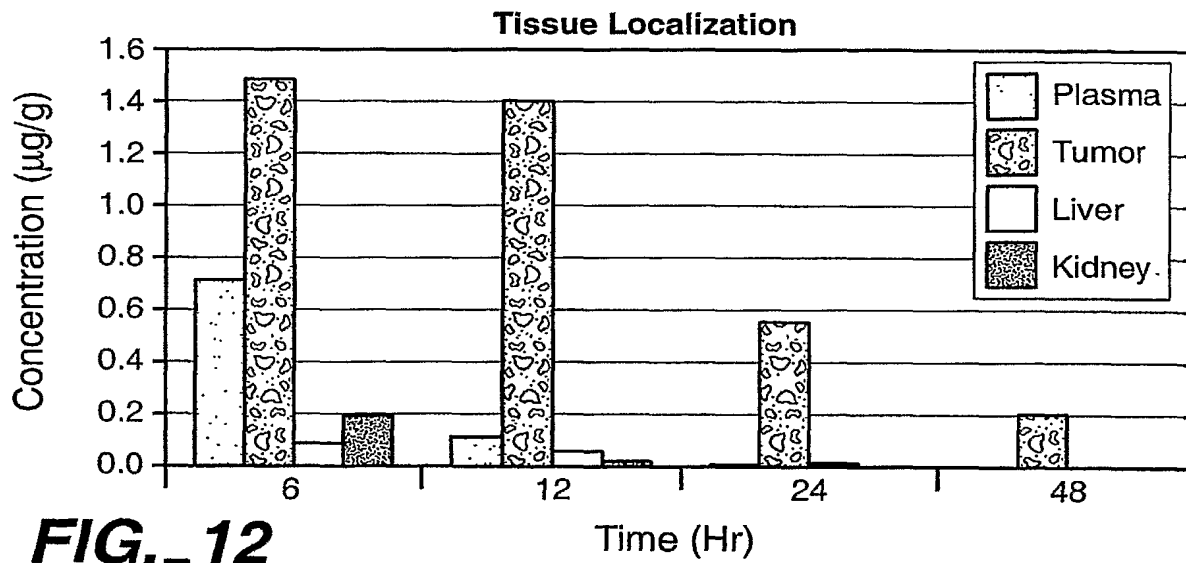
Lane 1: Molecular Weight Standard; Lanes 3-5: Unrelated Proteins; Lane 6: CAB1.11i.

**FIG.\_9**

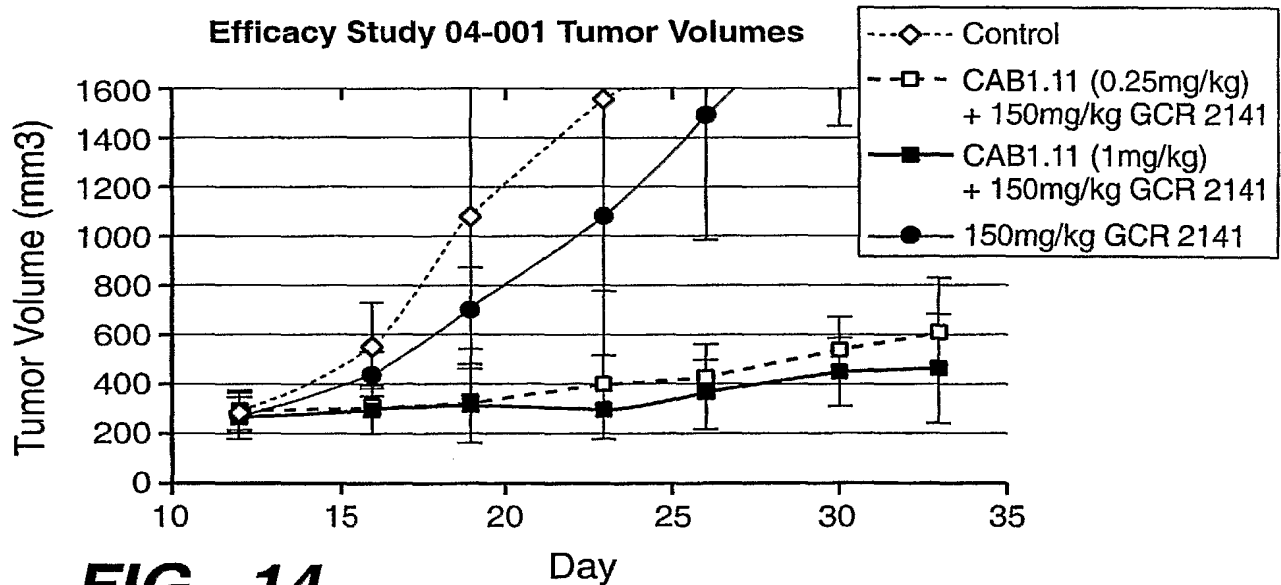
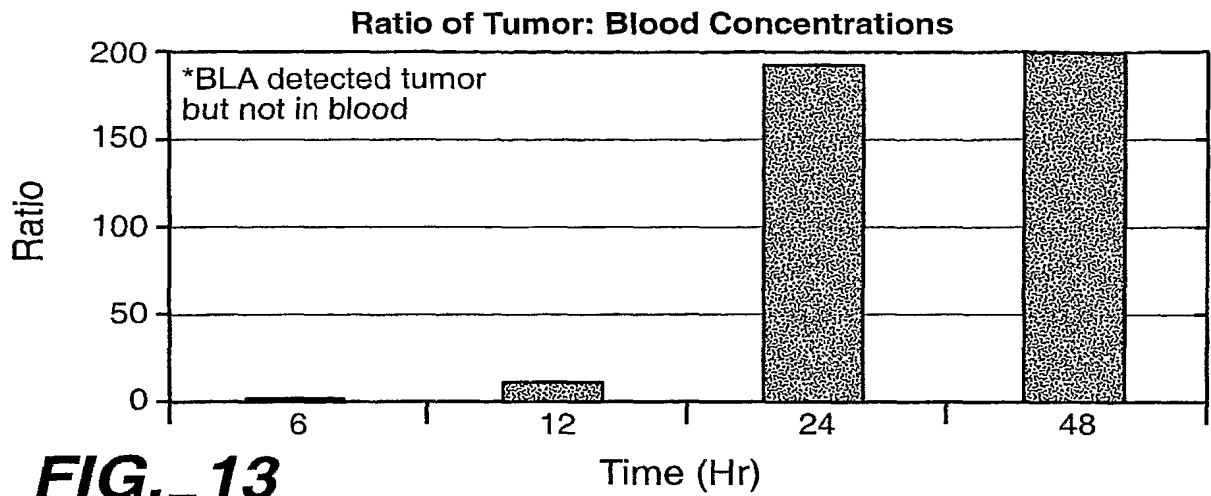
14 / 39

**FIG. 10A****FIG. 10B**

15 / 39

**FIG. 11****FIG. 12**

16 / 39





**FIG. 15A**

Case ID	ASM	Sample ID	Sample Pathology
<u>CI0000000255</u>	DF5	FR00005C7B	Adenocarcinoma of lung
<u>CI0000005496</u>	FF5	FR5B337147	Adenocarcinoma of lung
<u>CI0000011577</u>	FF1	FR5B34059F	Adenocarcinoma of lung
<u>CI7000000241</u>	AF4	FR00033A78	Adenocarcinoma of lung
<u>CI0000007518</u>	AF5	FR0001FD15	Carcinoma of lung, squamous cell
<u>CI0000008475</u>	HF4	FR65EE0784	Adenocarcinoma of colon, metastatic
<u>CI0000015252</u>	FF2	FR5B342166	Adenocarcinoma of colon

**FIG. 15B**

Case Diagnosis	Tissue of Origin/Site of Finding	H/E
Adenocarcinoma of lung Grade: AJCC G3: Poorly differentiated Stage: IIIA	Lung/Lung	<u>4X</u> <u>20X</u>
Adenocarcinoma of lung Grade: AJCC G3: Poorly differentiated Stage: IIIB	Lung/Lung	<u>4X</u> <u>20X</u>
Adenocarcinoma of lung Grade: AJCC G2: Moderately differentiated Stage: IIIA	Lung/Lung	<u>4X</u> <u>20X</u>
Adenocarcinoma of lung Grade: AJCC G2: Moderately differentiated Stage: IIIA	Lung/Lung	<u>4X</u> <u>20X</u>
Carcinoma of lung, squamous cell Grade: AJCC G3: Poorly differentiated Stage: IIIA	Lung/Lung	<u>4X</u> <u>20X</u>
Adenocarcinoma of colon, metastatic Grade: Not Reported Stage: IV	Colon/Liver	<u>4X</u> <u>20X</u>
Adenocarcinoma of colon Grade: AJCC G3: Poorly differentiated Stage: IIIB	Cecum/Cecum	<u>4X</u> <u>20X</u>

**FIG. 15C**

Anti-Human Cytokeratin AE1/AE3	CAB/GCR3708 (0.2ug/ml)
Immunogenicity: Tumor (100%, Variable to 3+ Cyto) Necrosis (Variable to 3+ EC) Specificity: High 4x <u>SF00029758</u> 20x	Immunogenicity: Tumor (100%, Variable to 3+ Cyto) Mixed inflammatory cells (Variable to 1+ Cyto) Specificity: High 4x <u>SF00029756</u> 20x
	Immunogenicity: Tumor (15%, Variable to 3+ Cyto) Intra-alveolar macrophages (Variable to 2+ Cyto) Mixed inflammatory cells (Variable to 2+ Cyto) Specificity: High 4x <u>SF0002975B</u> 20x
	Immunogenicity: Tumor (100%, 2+ Cyto) Cellular stroma (1+ Cyto) Chronic inflammatory cells (Variable to 1+ Cyto) Specificity: High 4x <u>SF0002977F</u> 20x
	Immunogenicity: Tumor (75%, Variable to 3+ Cyto) Cellular stroma (Variable to 2+ Cyto) Necrosis (Variable to 2+ EC) Intra-alveolar macrophages (Variable to 2+ Cyto) Specificity: High 4x <u>SF0002978B</u> 20x
	Immunogenicity: Tumor (100%, 3+ Cyto) Fibrotic stroma (1+ Cyto) Necrosis (Variable to 3+ EC) Specificity: High 4x <u>SF0002975F</u> 20x
Immunogenicity: Tumor (98%, Variable to 3+ Mem, Variable to 3+ Cyto) Fibrotic stroma (Variable to 1+ Cyto) Normal liver parenchyma (2+ Cyto) Necrosis (Variable to 3+ EC) Specificity: High 4x <u>SF0002976A</u> 20x	Immunogenicity: Tumor (95%, Variable to 3+ Mem, Variable to 3+ Cyto) Fibrotic stroma (Variable to 1+ Cyto) Normal liver parenchyma (1+ Cyto) Necrosis (Variable to 3+ EC) Specificity: High 4x <u>SF00029768</u> 20x Normal liver parenchyma shows positive staining (1+)
	Immunogenicity: Tumor (85%, Variable to 3+ Mem, Variable to 3+ Cyto) Cellular stroma (1+ Cyto) Normal muscle (Variable to 2+ Cyto) Specificity: High 4x <u>SF00029783</u> 20x

**FIG. 15D**

<b>CAB/GCR5517 (0.2ug/ml)</b>	<b>CAB/GCR6798 (0.2ug/ml)</b>
Immunogenicity: Tumor (100%, Variable to 3+ Cyto) Mixed inflammatory cells (Variable to 3+ Cyto) Necrosis (Variable to 2+ EC) Specificity: High <u>4x</u> <u>20x</u> <u>SF00029757</u>	Immunogenicity: Tumor (100%, Variable to 3+ Cyto) Mixed inflammatory cells (Variable to 1+ Cyto) Specificity: High <u>4x</u> <u>20x</u> <u>SF00029753</u>
Immunogenicity: Tumor (40%, Variable to 3+ Cyto) Intra-alveolar macrophages (Variable to 2+ Cyto) Mixed inflammatory cells (Variable to 2+ Cyto) Specificity: High <u>4x</u> <u>20x</u> <u>SF0002975C</u>	Immunogenicity: Tumor (10%, Variable to 2+ Cyto) Intra-alveolar macrophages (Variable to 2+ Cyto) Mixed inflammatory cells (Variable to 2+ Cyto) Specificity: High <u>4x</u> <u>20x</u> <u>SF00029759</u>
Immunogenicity: Tumor (100%, 2+ Cyto) Cellular stroma (1+ Cyto) Chronic inflammatory cells (Variable to 1+ Cyto) Specificity: High <u>4x</u> <u>20x</u> <u>SF00029780</u>	Immunogenicity: Tumor (100%, 2+ Cyto) Cellular stroma (1+ Cyto) Chronic inflammatory cells (Variable to 1+ Cyto) Specificity: High <u>4x</u> <u>20x</u> <u>SF0002977D</u>
Immunogenicity: Tumor (85%, Variable to 3+ Cyto) Cellular stroma (Variable to 2+ Cyto) Necrosis (Variable to 2+ EC) Intra-alveolar macrophages (Variable to 2+ Cyto) Specificity: High <u>4x</u> <u>20x</u> <u>SF0002978C</u>	Immunogenicity: Tumor (75%, Variable to 3+ Cyto) Cellular stroma (Variable to 2+ Cyto) Necrosis (Variable to 2+ EC) Intra-alveolar macrophages (Variable to 2+ Cyto) Specificity: High <u>4x</u> <u>20x</u> <u>SF00029789</u>
Immunogenicity: Tumor (100%, 3+ Cyto) Fibrotic stroma (1+ Cyto) Necrosis (Variable to 3+ EC) Specificity: High <u>4x</u> <u>20x</u> <u>SF00029760</u>	Immunogenicity: Tumor (100%, 3+ Cyto) Fibrotic stroma (1+ Cyto) Necrosis (Variable to 3+ EC) Specificity: High <u>4x</u> <u>20x</u> <u>SF0002975D</u>
Immunogenicity: Tumor (98%, Variable to 3+ Mem, Variable to 3+ Cyto) Fibrotic stroma (Variable to 1+ Cyto) Normal liver parenchyma (2+ Cyto) Necrosis (Variable to 3+ EC) Specificity: High <u>4x</u> <u>20x</u> <u>SF00029769</u>	Immunogenicity: Tumor (95%, Variable to 3+ Mem, Variable to 3+ Cyto) Fibrotic stroma (Variable to 1+ Cyto) Normal liver parenchyma (1+ Cyto) Necrosis (Variable to 3+ EC) Specificity: High <u>4x</u> <u>20x</u> <u>SF00029765</u> Normal liver parenchyma shows positive staining (1+)
Immunogenicity: Tumor (85%, Variable to 3+ Mem, Variable to 3+ Cyto) Cellular stroma (1+ Cyto) Normal muscle (Variable to 2+ Cyto) Specificity: High <u>4x</u> <u>20x</u> <u>SF00029784</u>	Immunogenicity: Tumor (95%, Variable to 3+ Mem, Variable to 3+ Cyto) Cellular stroma (1+ Cyto) Normal muscle (Variable to 2+ Cyto) Specificity: High <u>4x</u> <u>20x</u> <u>SF00029781</u>

**FIG. 15E**

<b>CAB/GCR8886 (0.196ug/ml)</b>	<b>No Antibody Control (Prediluted)</b>
Immunogenicity: Tumor (100%, Variable to 3+ Cyto) Mixed inflammatory cells (Variable to 1+ Cyto) Specificity: High <div>4x<div>SF00029754</div>20x</div>	Immunogenicity: N/A Specificity: Unknown <div>SF00029755</div>
Immunogenicity: Tumor (10%, Variable to 2+ Cyto) Intra-alveolar macrophages (Variable to 2+ Cyto) Mixed inflammatory cells (Variable to 2+ Cyto) Specificity: High <div>4x<div>SF0002975A</div>20x</div>	
Immunogenicity: Tumor (100%, 2+ Cyto) Cellular stroma (1+ Cyto) Chronic inflammatory cells (Variable to 1+ Cyto) Specificity: High <div>4x<div>SF0002977E</div>20x</div>	
Immunogenicity: Tumor (75%, Variable to 3+ Cyto) Cellular stroma (Variable to 2+ Cyto) Necrosis (Variable to 2+ EC) Intra-alveolar macrophages (Variable to 2+ Cyto) Specificity: High <div>4x<div>SF0002978A</div>20x</div>	
Immunogenicity: Tumor (100%, 3+ Cyto) Fibrotic stroma (1+ Cyto) Necrosis (Variable to 3+ EC) Specificity: High <div>4x<div>SF0002975E</div>20x</div>	
Immunogenicity: Tumor (95%, Variable to 3+ Mem, Variable to 3+ Cyto) Fibrotic stroma (Variable to 1+ Cyto) Normal liver parenchyma (1+ Cyto) Necrosis (Variable to 3+ EC) Specificity: High <div>4x<div>SF00029766</div>20x</div> Normal liver parenchyma shows positive staining (1+)	Immunogenicity: N/A Specificity: Unknown <div>SF00029767</div>
Immunogenicity: Tumor (95%, Variable to 3+ Mem, Variable to 3+ Cyto) Cellular stroma (1+ Cyto) Normal muscle (Variable to 2+ Cyto) Specificity: High <div>4x<div>SF00029782</div>20x</div>	

22 / 39			
<u>CI0000017970</u>	HF1	FR65EE7B3D	Adenocarcinoma of colon
<u>CI0000010013</u>	AF2	FR00028F2E	Adenocarcinoma of pancreas, metastatic
<u>CI0000009651</u>	AF1	FR0002B111	Adenocarcinoma of pancreas, ductal
<u>CI0000008690</u>	CF4	FR00027B0E	Adenocarcinoma of pancreas, ductal
<u>CI0000007678</u>	AF3	FR0002575B	Adenocarcinoma of pancreas, ductal
<u>CI0000009736</u>	AF2	FR0002BAB4	Adenocarcinoma of pancreas, ductal

**FIG. 15F**



23 / 39

Adenocarcinoma of colon Grade: AJCC G3: Moderately differentiated Stage: IIIC	Colon/Colon	<u>4X</u> <u>20X</u>
Adenocarcinoma of pancreas, metastatic Grade: Not Reported Stage: IV	Pancreas/Omentum	<u>4X</u> <u>20X</u>
Adenocarcinoma of pancreas, ductal Grade: AJCC G2: Moderately differentiated Stage: IIB	Pancreas/Pancreas	<u>4X</u> <u>20X</u>
Adenocarcinoma of pancreas, ductal Grade: AJCC G1: Well differentiated Stage: IIA	Pancreas/Pancreas	<u>4X</u> <u>20X</u>
Adenocarcinoma of pancreas, ductal Grade: AJCC G2: Moderately differentiated Stage: III	Pancreas/Pancreas	<u>4X</u> <u>20X</u>
Adenocarcinoma of pancreas, ductal Grade: AJCC G2: Moderately differentiated Stage: IIB	Pancreas/Pancreas	<u>4X</u> <u>20X</u>

**FIG. 15G**

24 / 39

	<p>Immunogenicity: Tumor (100%, 3+ Cyto) Cellular stroma (1+ Cyto) Necrosis (Variable to 3+ EC) Specificity: High</p> <p><u>4x</u> <u>20x</u></p> <p><u>SF00029787</u></p>
<p>Immunogenicity: Tumor (100%, 3+ Cyto) Fibroadipose tissue (Variable to 1+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u></p> <p><u>SF0002977C</u></p>	<p>Immunogenicity: Tumor (100%, 3+ Cyto) Fibroadipose tissue (Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u></p> <p><u>SF0002977A</u></p>
	<p>Immunogenicity: Tumor (100%, 3+ Cyto) Desmoplastic stroma (Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u></p> <p><u>SF00029771</u></p>
	<p>Immunogenicity: Tumor (100%, 3+ Cyto) Myxoid stroma (Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u></p> <p><u>SF0002976D</u></p>
	<p>Immunogenicity: Tumor (85%, Variable to 3+ Cyto) Cellular stroma (Variable to 1+ Cyto) Chronic pancreatitis (Variable to 1+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u></p> <p><u>SF00029763</u></p>
	<p>Immunogenicity: Tumor (100%, 3+ Cyto) Chronic pancreatitis (Variable to 2+ Cyto) Fibrotic stroma (Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u></p> <p><u>SF00029775</u></p>

**FIG.\_15H**



25 / 39

<p>Immunogenicity: Tumor (100%, 3+ Cyto) Cellular stroma (1+ Cyto) Necrosis (Variable to 3+ EC) Specificity: High</p> <p><u>4x</u> <u>20x</u></p> <p><u>SF00029788</u></p>	<p>Immunogenicity: Tumor (100%, 3+ Cyto) Cellular stroma (1+ Cyto) Necrosis (Variable to 3+ EC) Specificity: High</p> <p><u>4x</u> <u>20x</u></p> <p><u>SF00029785</u></p>
<p>Immunogenicity: Tumor (100%, 3+ Cyto) Fibroadipose tissue (Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u></p> <p><u>SF0002977B</u></p>	<p>Immunogenicity: Tumor (100%, 3+ Cyto) Fibroadipose tissue (Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u></p> <p><u>SF00029777</u></p>
<p>Immunogenicity: Tumor (100%, 3+ Cyto) Desmoplastic stroma (Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u></p> <p><u>SF00029772</u></p>	<p>Immunogenicity: Tumor (100%, 3+ Cyto) Desmoplastic stroma (Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u></p> <p><u>SF00029770</u></p>
<p>Immunogenicity: Tumor (100%, 3+ Cyto) Myxoid stroma (Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u></p> <p><u>SF0002976E</u></p>	<p>Immunogenicity: Tumor (100%, 3+ Cyto) Myxoid stroma (Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u></p> <p><u>SF0002976B</u></p>
<p>Immunogenicity: Tumor (85%, Variable to 3+ Cyto) Cellular stroma (Variable to 1+ Cyto) Chronic pancreatitis (Variable to 1+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u></p> <p><u>SF00029764</u></p>	<p>Immunogenicity: Tumor (85%, Variable to 3+ Cyto) Cellular stroma (Variable to 1+ Cyto) Chronic pancreatitis (Variable to 1+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u></p> <p><u>SF00029761</u></p>
<p>Immunogenicity: Tumor (100%, 3+ Cyto) Chronic pancreatitis (Variable to 2+ Cyto) Fibrotic stroma (Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u></p> <p><u>SF00029776</u></p>	<p>Immunogenicity: Tumor (100%, 3+ Cyto) Chronic pancreatitis (Variable to 1+ Cyto) Fibrotic stroma (Variable to 1+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u></p> <p><u>SF00029773</u></p>

**FIG. 15I**

26 / 39

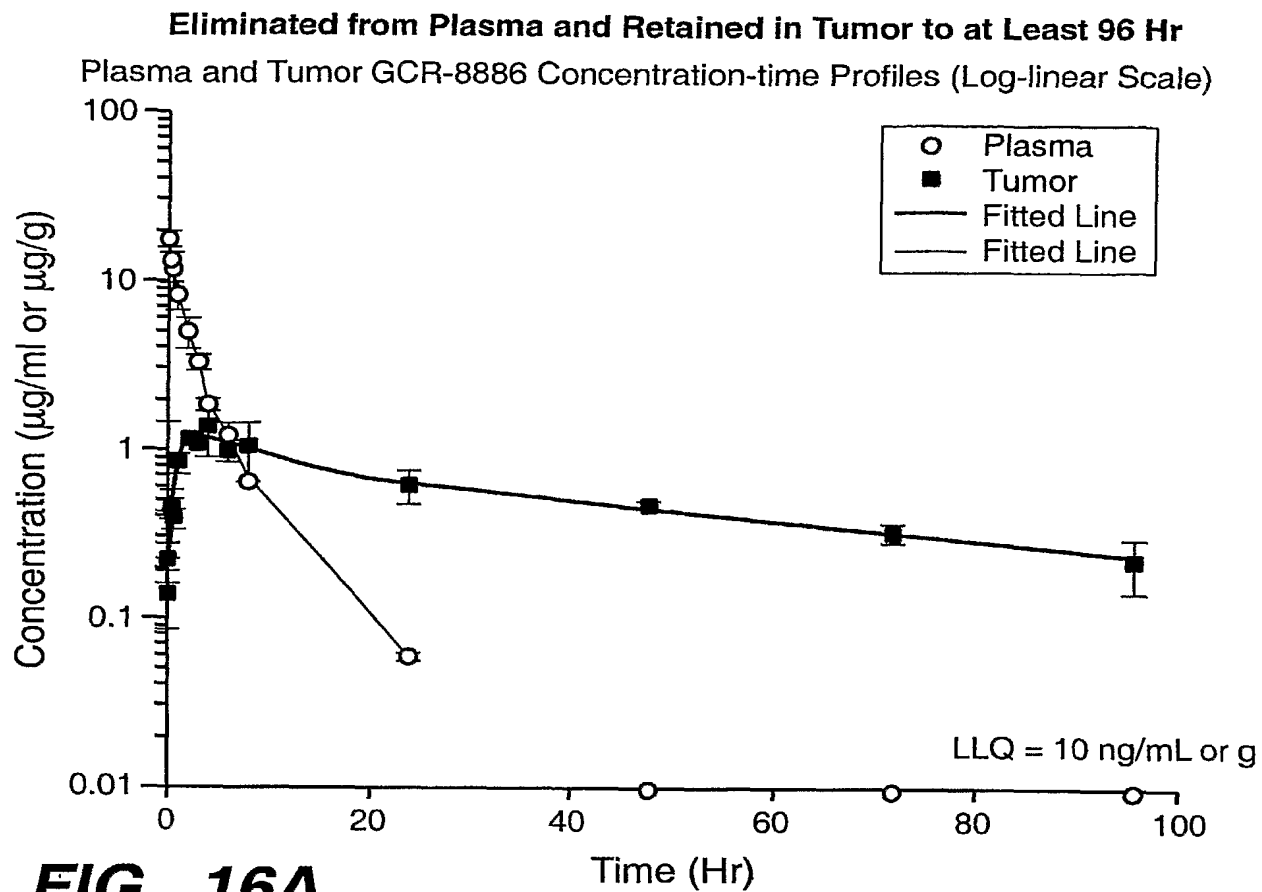
<p>Immunogenicity: Tumor (100%, 3+ Cyto) Cellular stroma (1+ Cyto) Necrosis (Variable to 3+ EC) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF00029786</u></p>	
<p>Immunogenicity: Tumor (100%, 3+ Cyto) Fibroadipose tissue (Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF00029778</u></p>	<p>Immunogenicity: N/A Specificity: N/A</p> <p><u>SF00029779</u></p>
<p>Immunogenicity: Tumor (100%, 3+ Cyto) Desmoplastic stroma (Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF0002976F</u></p>	
<p>Immunogenicity: Tumor (100%, 3+ Cyto) Myxoid stroma (Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF0002976C</u></p>	
<p>Immunogenicity: Tumor (85%, Variable to 3+ Cyto) Cellular stroma (Variable to 1+ Cyto) Chronic pancreatitis (Variable to 1+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF00029762</u></p>	
<p>Immunogenicity: Tumor (100%, 3+ Cyto) Chronic pancreatitis (Variable to 2+ Cyto) Fibrotic stroma (Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF00029774</u></p>	

**FIG.\_15J**

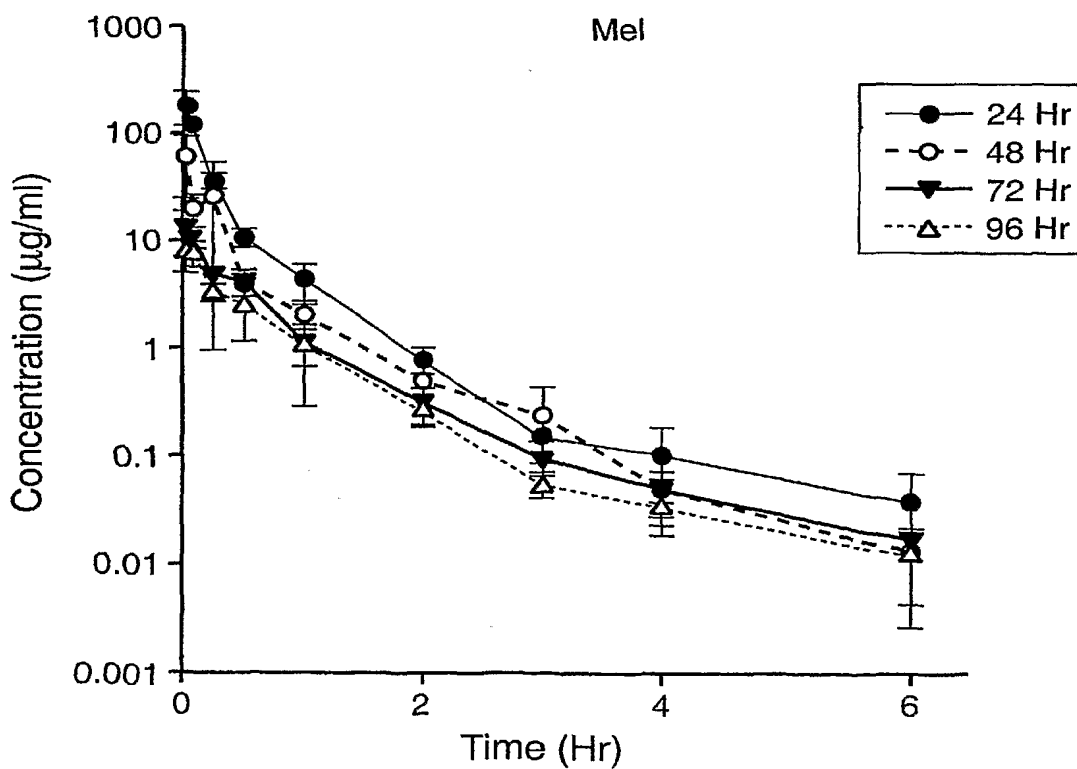
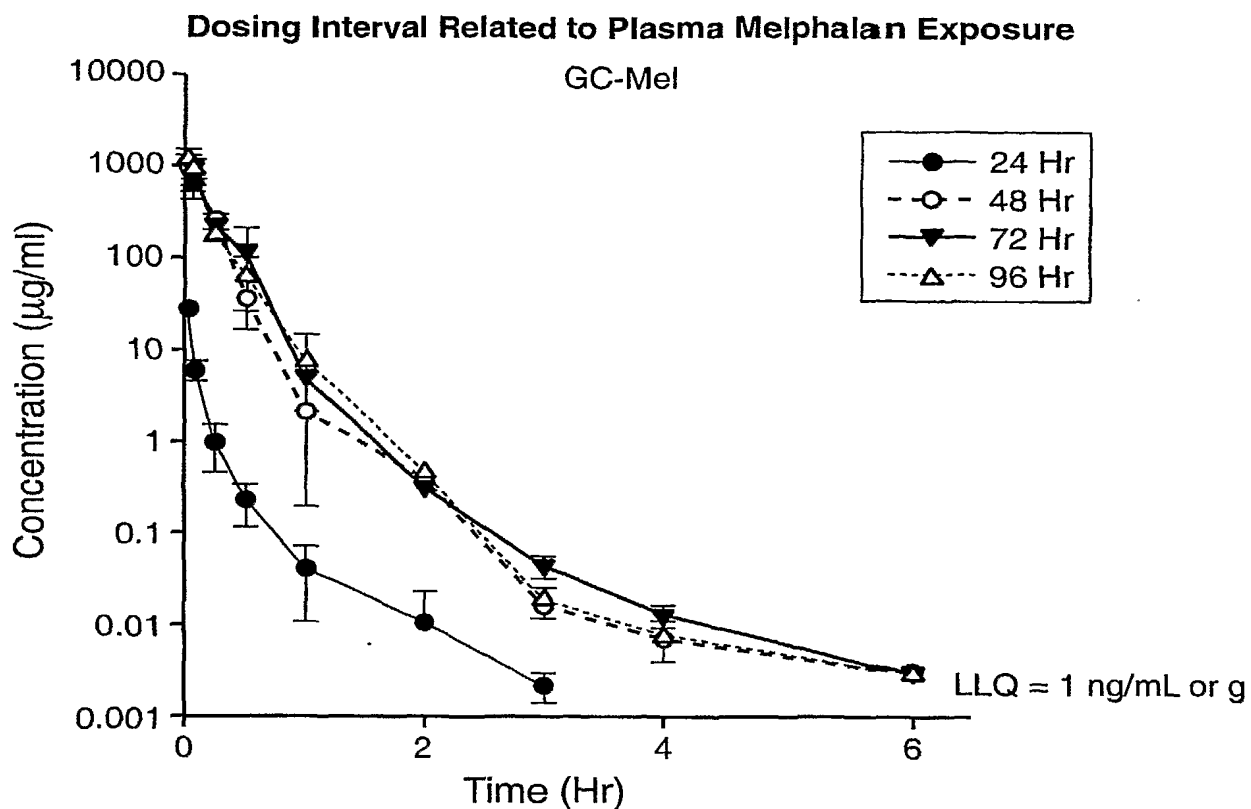
<b>FIG._15A</b>	<b>FIG._15B</b>	<b>FIG._15C</b>	<b>FIG._15D</b>	<b>FIG._15E</b>
<b>FIG._15F</b>	<b>FIG._15G</b>	<b>FIG._15H</b>	<b>FIG._15I</b>	<b>FIG._15J</b>

**FIG.\_15**

27 / 39

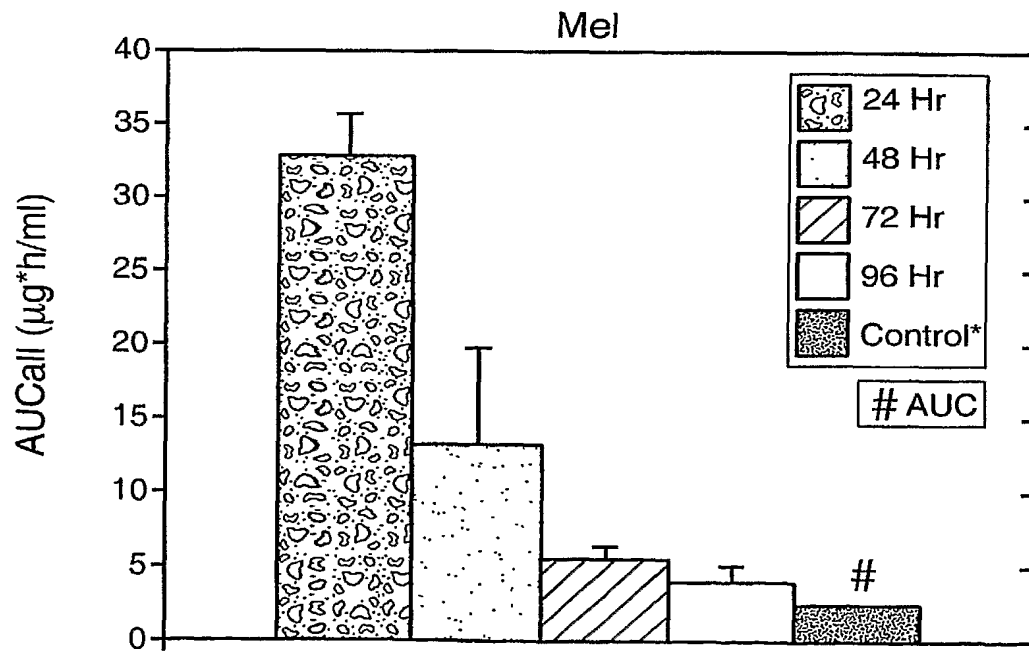
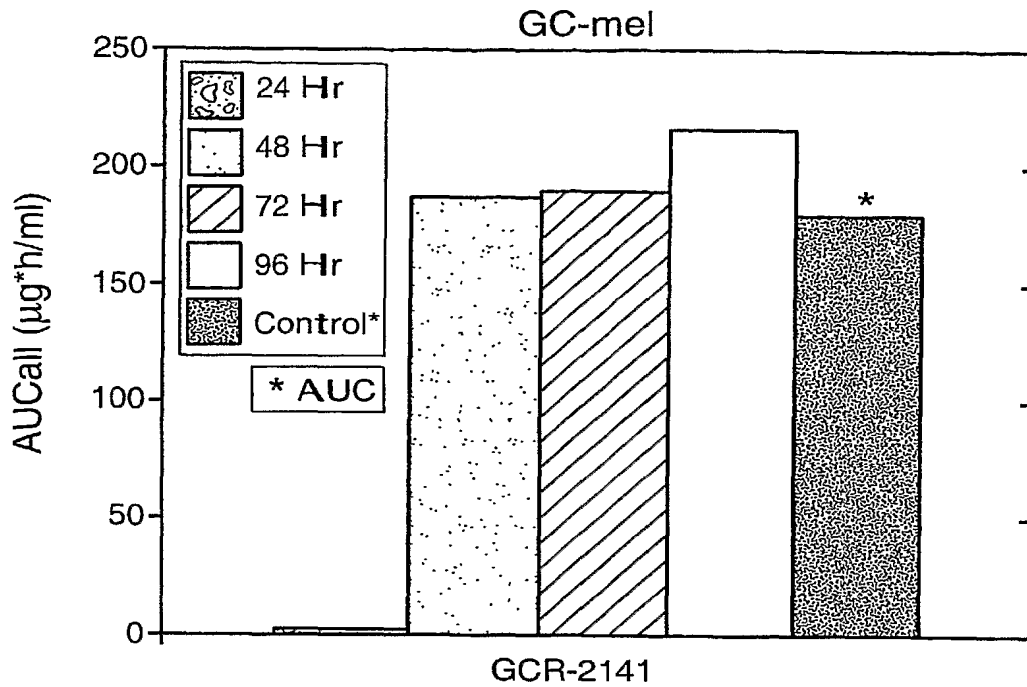
**FIG. 16A**

28 / 39

**FIG. 16B-1**

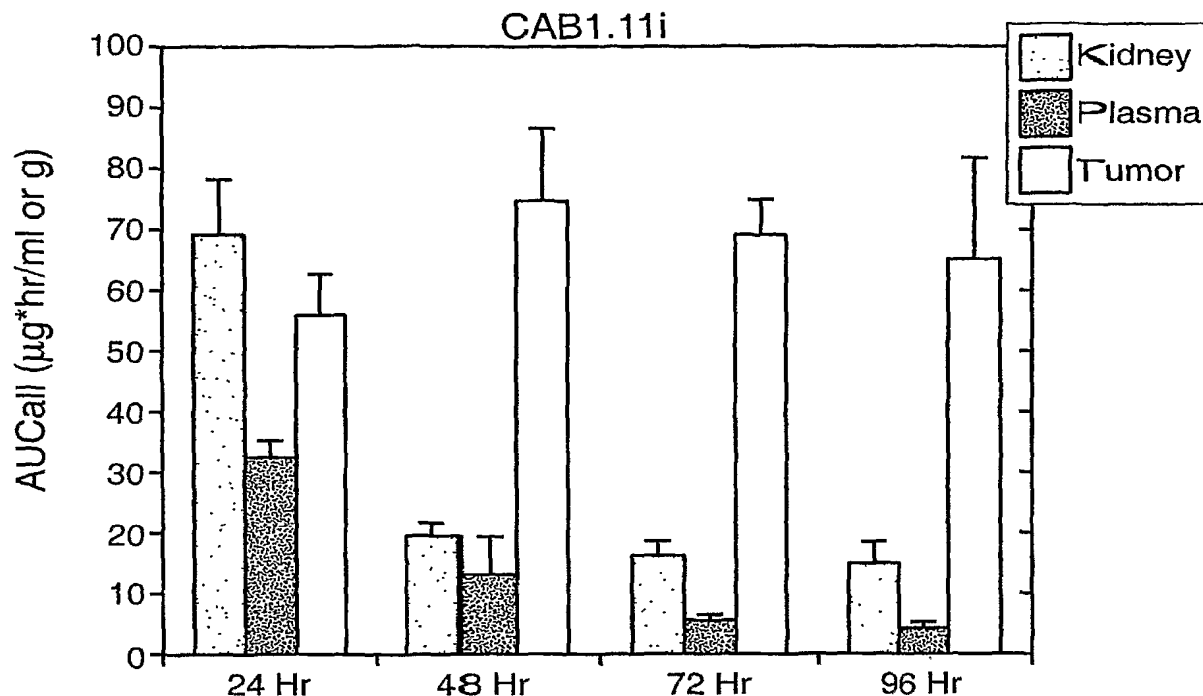
29 / 39

## Dosing Interval Related to Plasma Melphalan Exposure

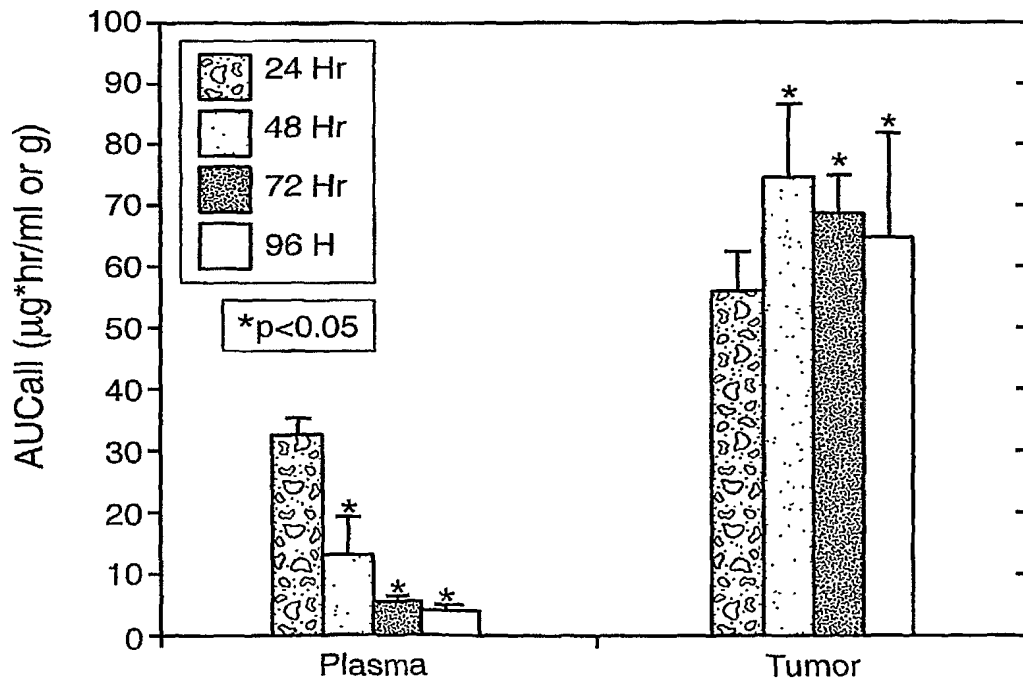
**FIG. 16B-2**

30 / 39

**Plasma and Kidney Exposure to is Decreased with Increased Interval Between GCR CAB1.11i and GCR GC-mel Administration**

**FIG. 17**

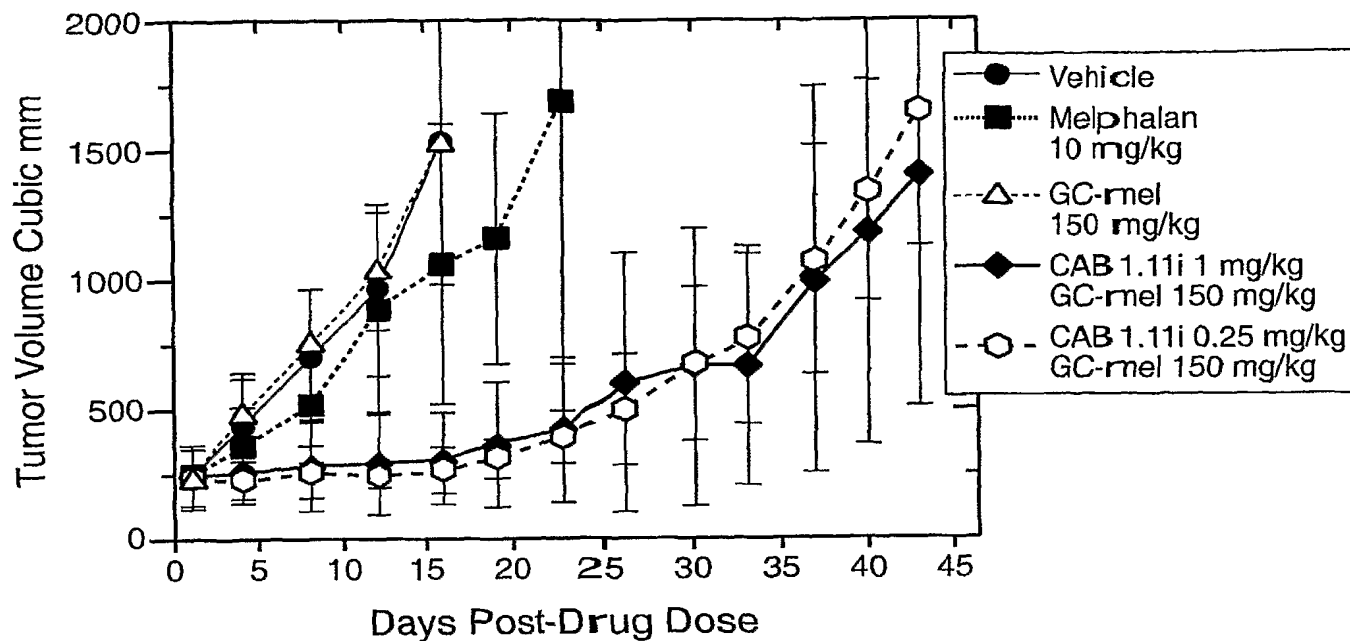
**Efficacious Tumor Melphalan Exposures Achieved at Each Time Interval While Systemic Melphalan Exposure Decreased**



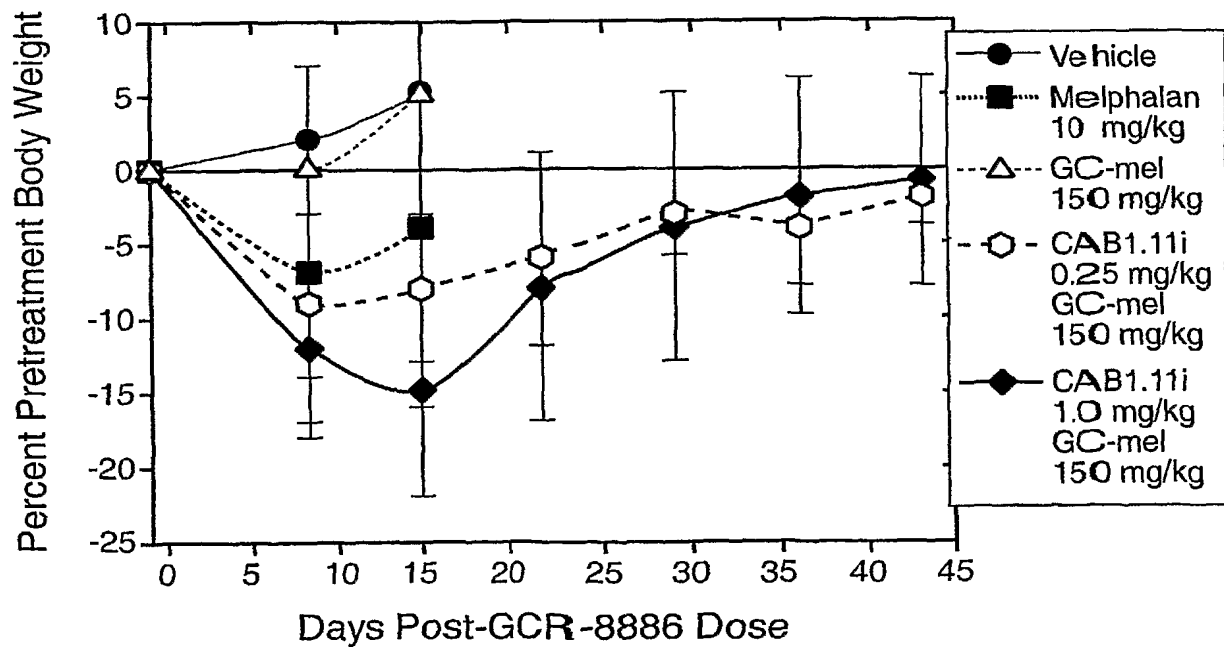
• Efficacy demonstrated at 24 hr interval in TLS174T xenograft mouse model

**FIG. 18**

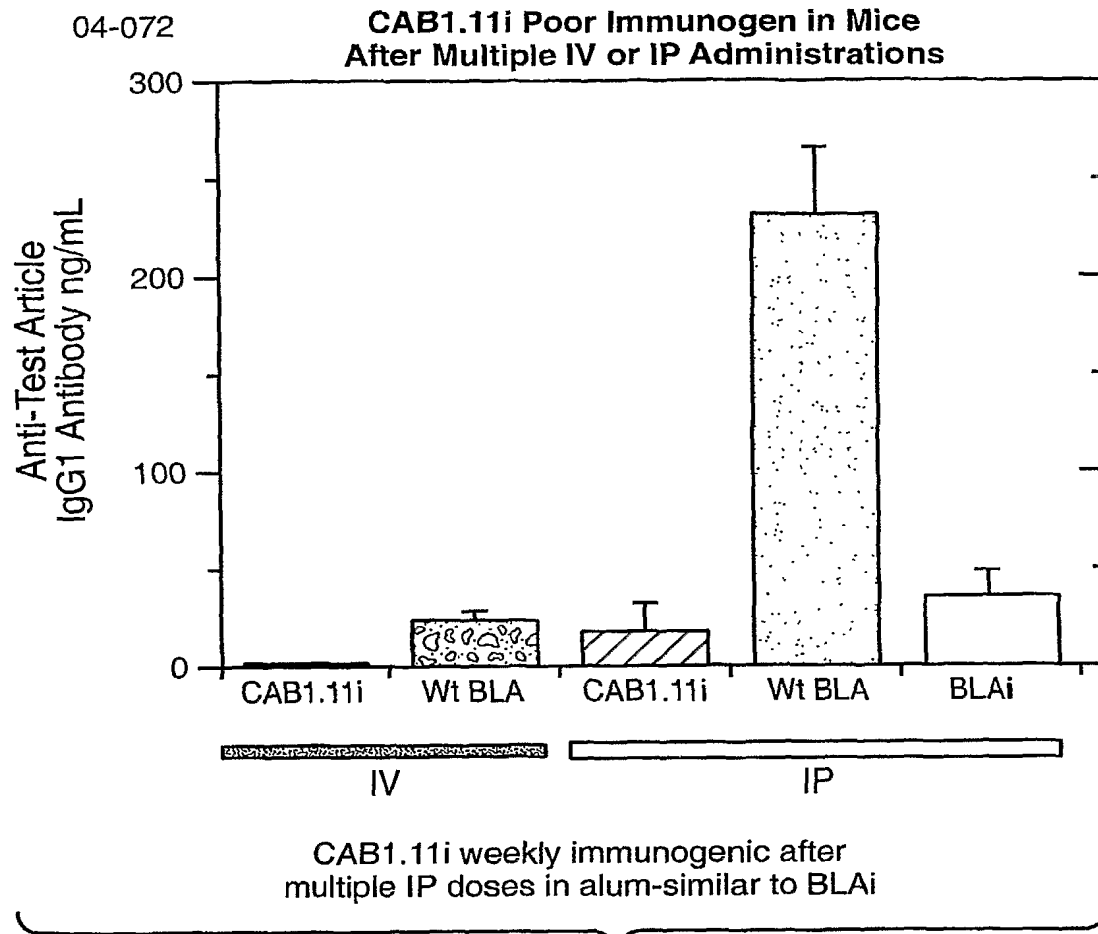
31 / 39

**FIG. 19A**

04-066 Completed

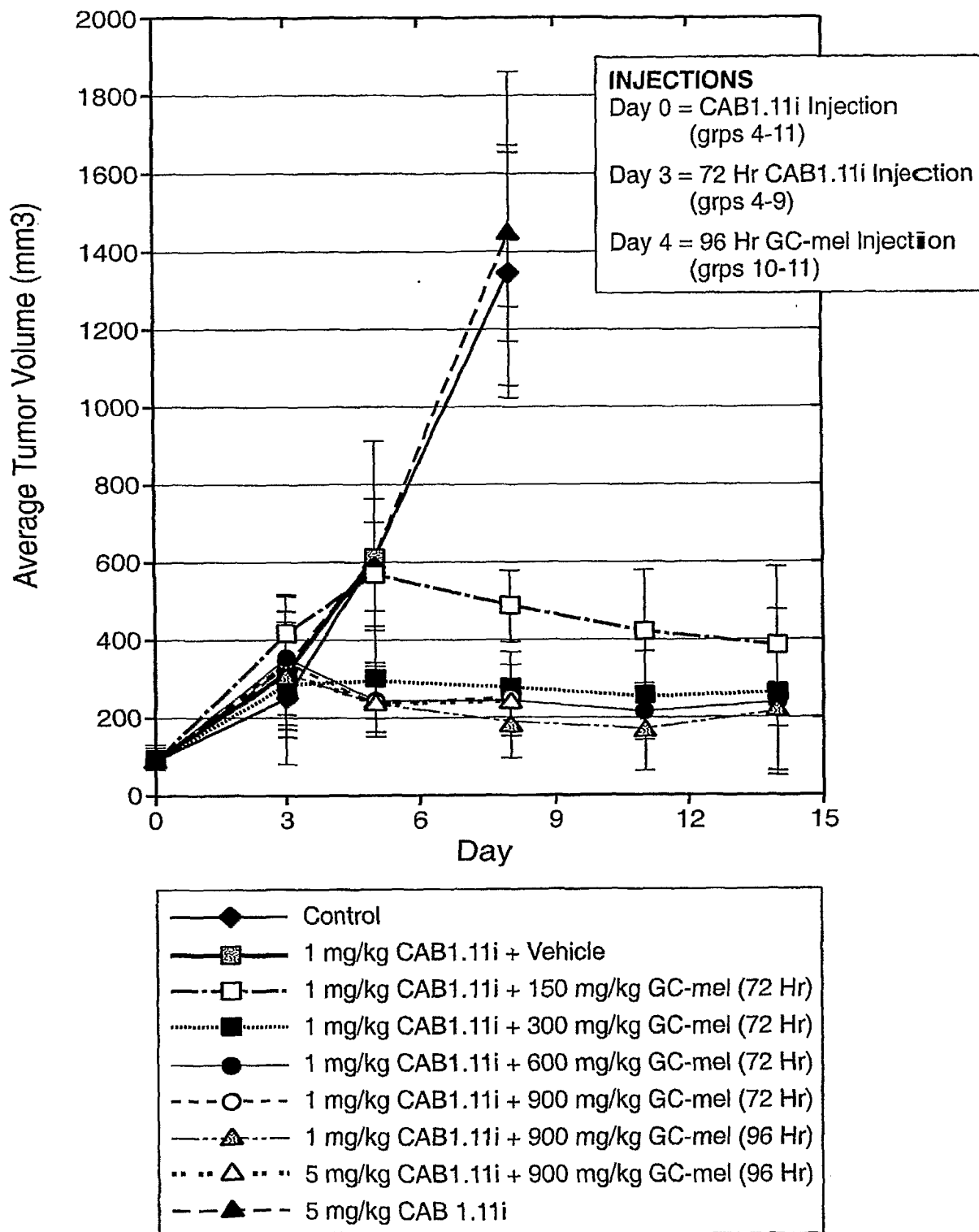
**FIG. 19B**

32 / 39

**FIG. 20**

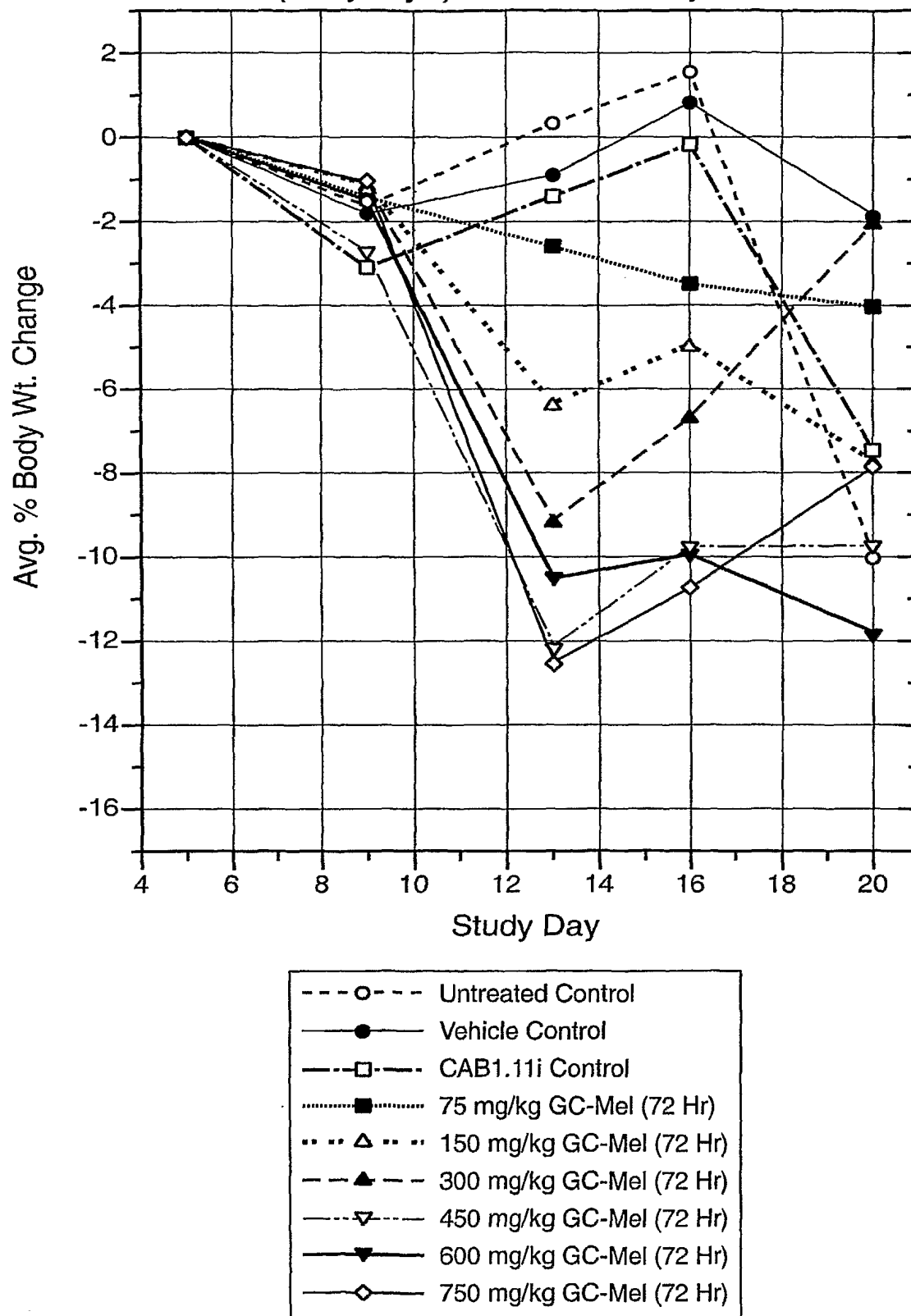


33 / 39

**FIG. 21**

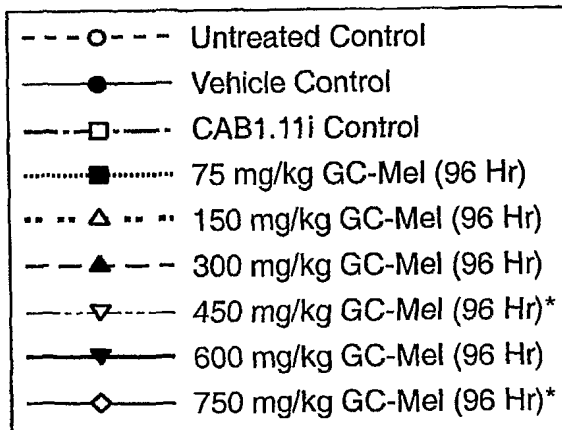
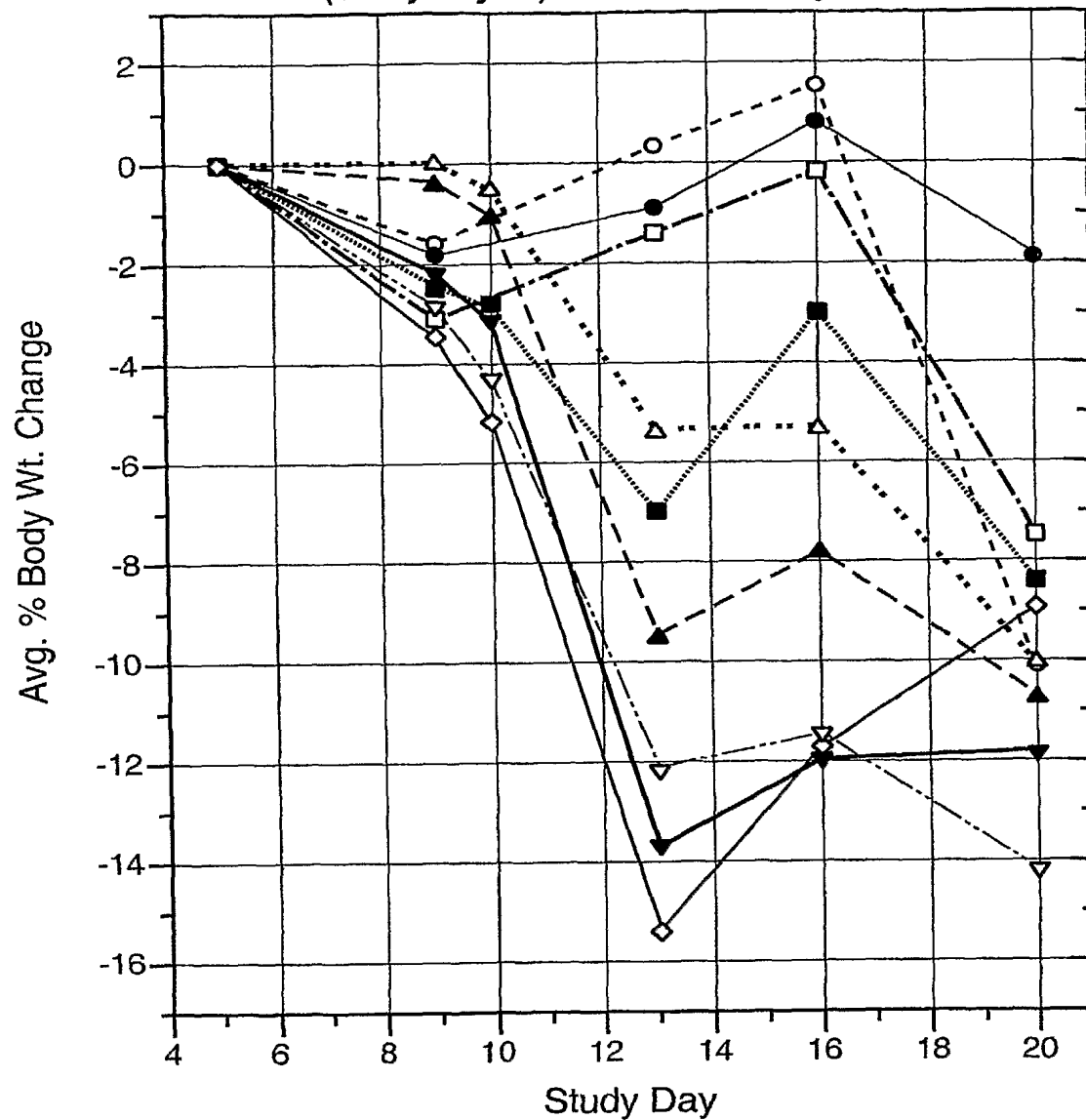
34 / 39

Avg. % Body Wt. Loss – GC-mel Injection 72 Hrs.  
(Study Day 9) Post GCR-8886 Injection

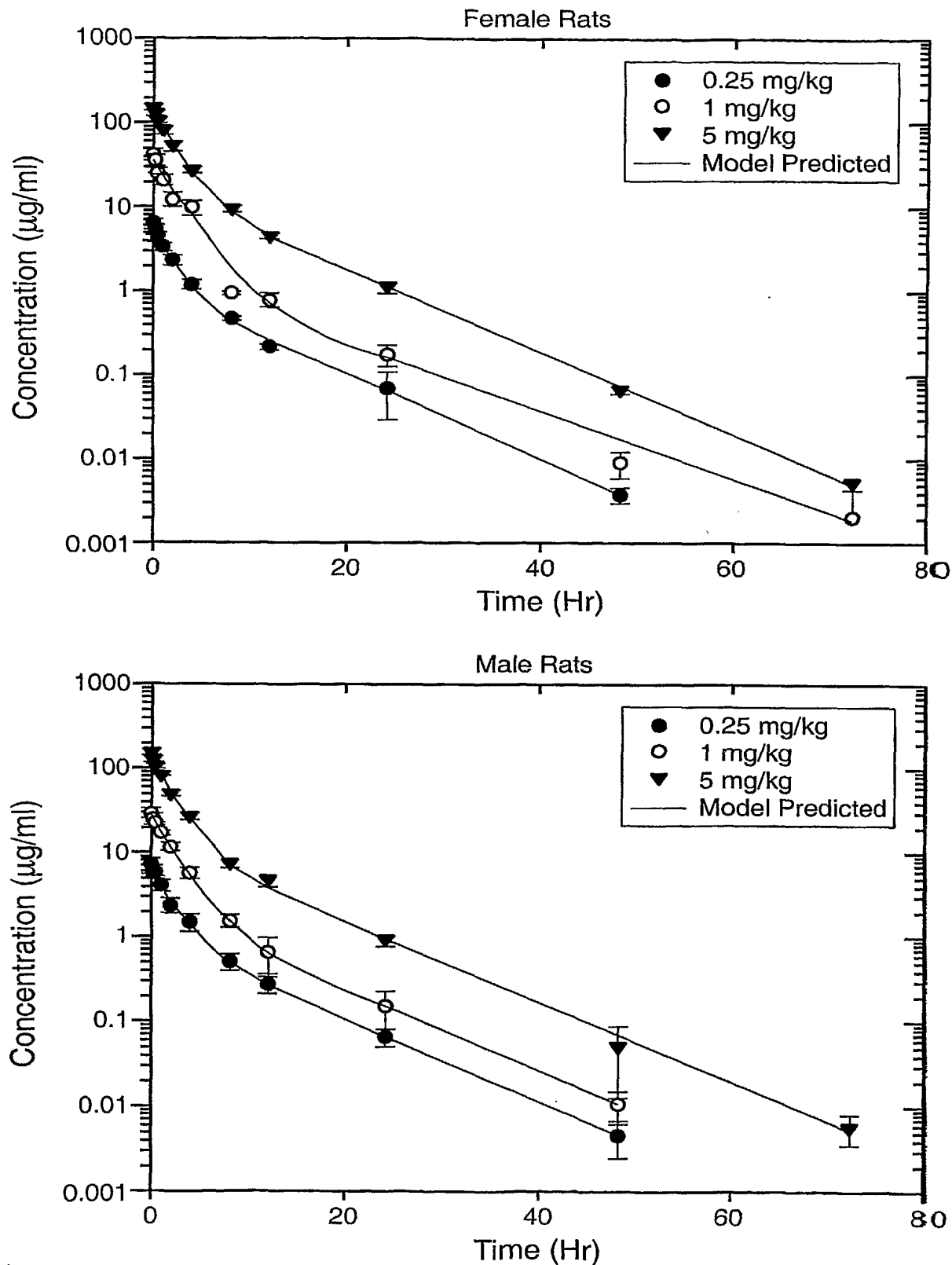
**FIG. 22A**

35 / 39

Avg. % Body Wt. Loss – GC-mel Injection 96 Hrs.  
(Study Day 10) Post CAB1.11i Injection

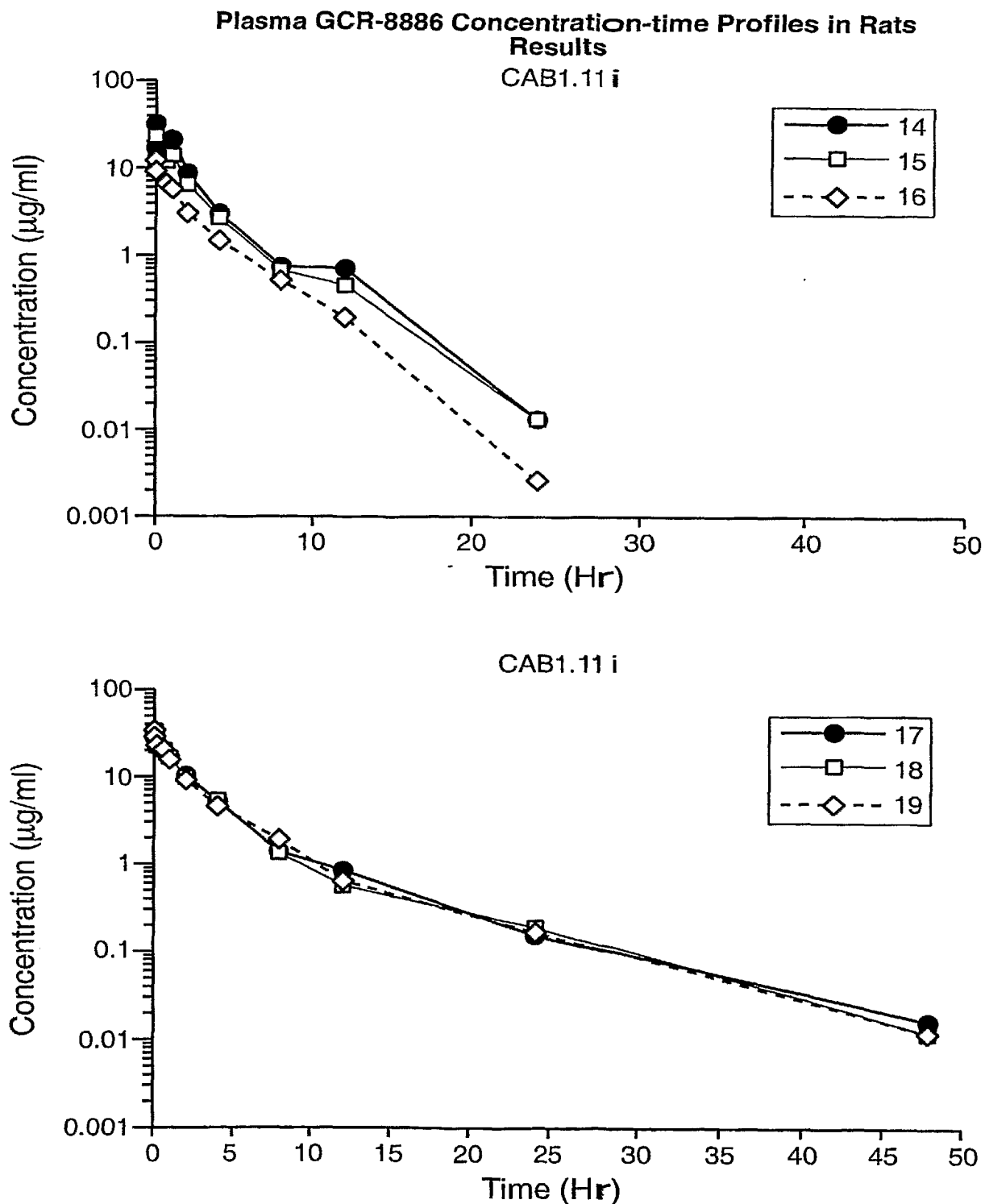
**FIG. 22B**

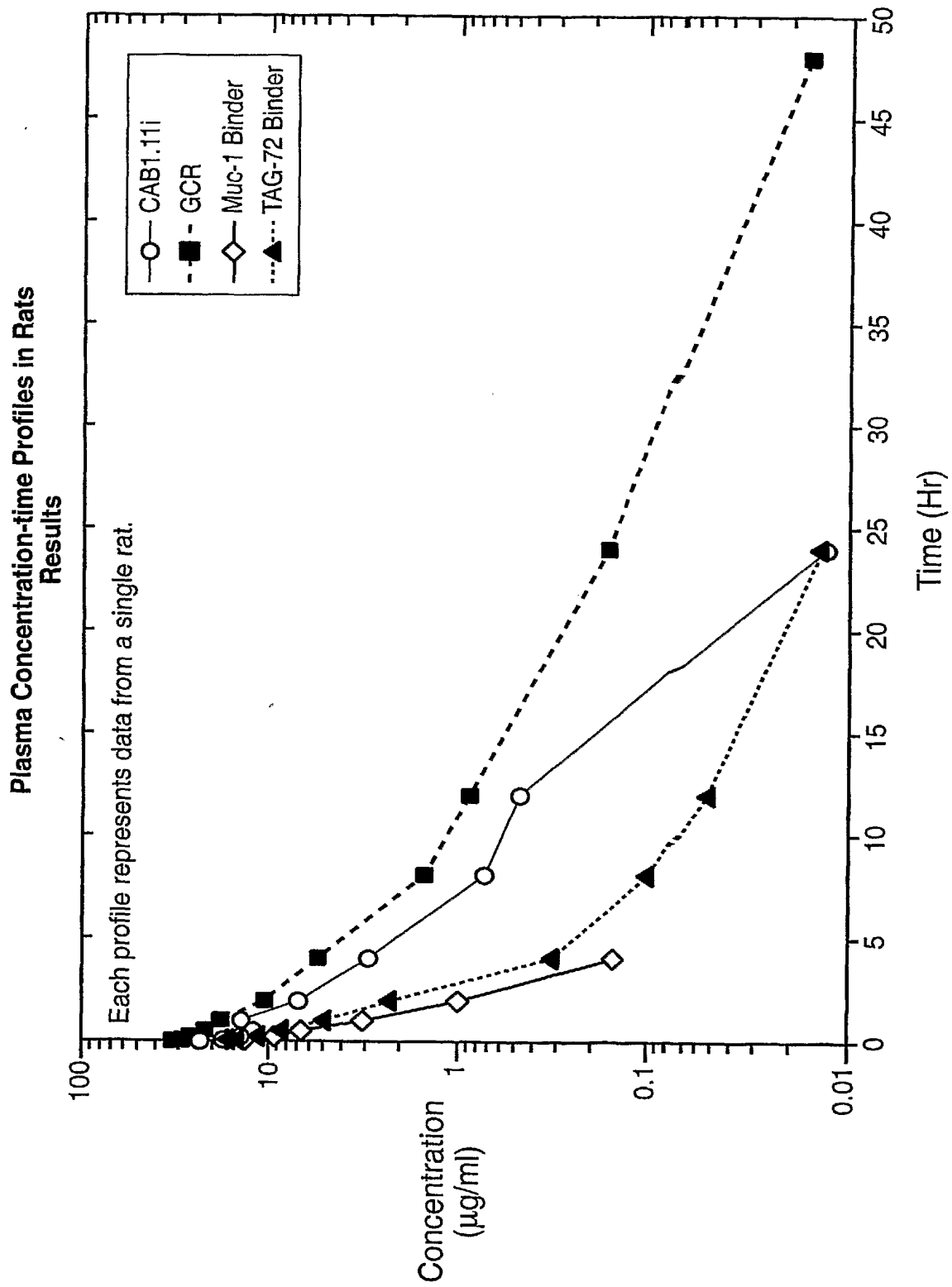
36 / 39

**Plasma CAB1.11i Concentration-time Profile in Rats  
Results****FIG. 23**

SUBSTITUTE SHEET (RULE 26)

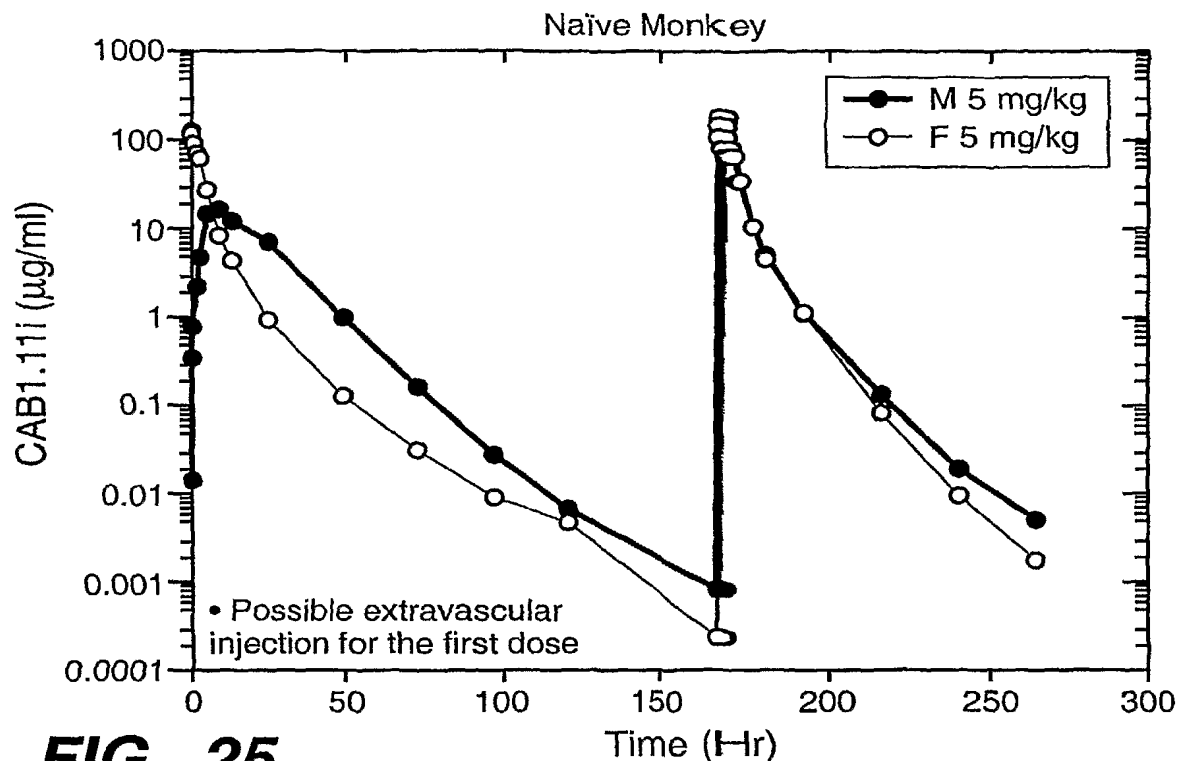
37 / 39

**FIG. 24A**

**FIG. 24B**

39 / 39

### GCR-8886 Concentration-time Profiles Following 2 Weekly Doses Results



### CAB1.11i PK Parameter Estimates with or without CEA Coadministration Results

